Package: rcosmo (via r-universe)

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Title Cosmic Microwave Background Data Analysis

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Description Tools for handling and analysing spherical data on a HEALPix grid, with applications to cosmic microwave background maps. Supports reading FITS files, converting between spherical and Cartesian coordinates and HEALPix ordering schemes, selecting sky regions, sampling pixels, and visualising maps. Implements empirical covariance, correlation and variogram estimation, covariance model fitting, angular power spectrum estimation, and distributional and entropy-based comparisons of spherical data. The package and its methods are described by Fryer, Li and Olenko (2020) <doi:10.32614/RJ-2020-012>.

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`ancestor` *Return index of kth ancestor pixel*

Description

Gives the pixel at resolution $j - k$ that contains p, where p is specified at resolution j (notice it does not depend on j).

Usage

```
ancestor(p, k)
```

Arguments

`p`	A pixel index specified in nested order.
`k`	A generation of an ancestor pixel.

Value

A numeric vector of nested pixel indices at resolution $j - k$, identifying the ancestors containing the input pixels.

Examples

```
ancestor(4,2)
ancestor(17,2)
```

areCompatibleCMBDFs *Check compatibleness of CMBDataFrames*

Description

Compare attributes to decide if two CMBDataFrames are compatible

Usage

```
areCompatibleCMBDFs(cmbdf1, cmbdf2, compare.pix = FALSE)
```

Arguments

cmbdf1	a CMBDataFrame
cmbdf2	a CMBDataFrame
compare.pix	A boolean. If TRUE then cmbdf1 and cmbdf2 must share the same pixel indices to be considered compatible

Details

If the CMBDataFrames do not have compatible attributes then a message is printed indicating the attributes that do not match. To suppress this use the suppressMessages function

Value

A single logical value, TRUE if both objects have the same nside and ordering, and also the same pixel indices when compare.pix = TRUE; otherwise FALSE. Incompatibilities are reported with a suppressible message.

Examples

```
a <- CMBDataFrame(nside = 2, ordering = "ring", coords = "cartesian")
b <- CMBDataFrame(nside = 1, ordering = "nested", coords = "spherical")
areCompatibleCMBDFs(a,b)

suppressMessages(areCompatibleCMBDFs(a,b))
```

as.CMBDataFrame *Convert objects to* CMBDataFrame

Description

Safely converts a data.frame to a CMBDataFrame. The rows of the data.frame are assumed to be in the HEALPix order given by ordering, and at the HEALPix resolution given by nside. Coordinates, if present, are assumed to correspond to HEALPix pixel centers. The coordinates must be named either x,y,z (cartesian) or theta, phi (spherical colatitude and longitude respectively). If df is a HPDataFrame then it is possible that df has attribute healpixCentered = TRUE, in which case as.CMBDataFrame will perform HEALPix centering of coordinates.

Usage

```
as.CMBDataFrame(df, ordering, nside, spix, drop.coords = FALSE)
```

Arguments

df	Any data.frame or HPDataFrame whose rows are in HEALPix order
ordering	character string that specifies the ordering scheme ("ring" or "nested")
nside	an integer 2^k that specifies the Nside (resolution) HEALPix parameter
spix	an integer vector that specifies the HEALPix pixel index corresponding to each row of df. If spix is left blank and df is a data.frame, then df is assumed to contain data for every pixel at resolution parameter nside (the full sky). In other words, in this case, the number of rows of df must be equal to 12*nside^2. However, if spix is left blank and df is a CMBDataFrame, then spix is set equal to pix(df)
drop.coords	A logical. If df is a HPDataFrame then it is possible that df has attribute healpixCentered = TRUE, in which case as.CMBDataFrame will perform HEALPix centering of coordinates. If drop.coords = TRUE then this will be done by dropping existing coordinates entirely (quicker) to rely only on HEALPix pixel indices. Otherwise if drop.coords = FALSE this will be done by replacing existing coordinates with locations of HEALPix pixel centers.

Value

A CMBDataFrame

Examples

```
## Example 1: Create df with no coords, then create CMBDataFrames cmbdf and
## df2 with spherical coords

df <- data.frame(I=rnorm(12))
df

cmbdf <- as.CMBDataFrame(df,ordering= "ring", nside=1)
```

```
summary(cmbdf)
pix(cmbdf)
coords(cmbdf)

df2 <- coords(cmbdf, new.coords = "spherical")
df2

## Example 2: Create CMBDataFrames for first 10 Healpix centers

df <- data.frame(I=rnorm(10))
df
cmbdf <- as.CMBDataFrame(df,ordering= "ring", nside=2, spix=1:10)
summary(cmbdf)
pix(cmbdf)
```

---

assumedConvex *Check if a* CMBWindow *is assumed convex.*

Description

Initially any CMBWindow is not assumed convex. The assumedConvex attribute can be change for any CMBWindow.

Usage

```
assumedConvex(win, assume.convex)
```

Arguments

win	a CMBWindow object
assume.convex	optionally change the assumedConvex attribute to TRUE or FALSE

Value

A logical value giving the convexity assumption when assume.convex is omitted; otherwise the CMBWindow with its convexity attribute updated.

Examples

```
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
assumedConvex(win1)
win2 <- assumedConvex(win1, assume.convex = TRUE)
assumedConvex(win2)
assumedConvex(win1) <- TRUE
assumedConvex(win1)
```

assumedUniquePix *Check if object was assumed to have unique HEALPix indices*

Description

The function checks object's attribute assumedUniquePix. The attribute is True if the object was assumed to have rows that correspond to unique HEALPix pixel indices.

Usage

```
assumedUniquePix(obj)
```

Arguments

obj	Any object.

Value

A boolean. This is TRUE if obj is a CMBDataFrame or a HPDataFrame whose rows were assumed to correspond to unique HEALPix pixel indices.

Examples

```
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)
coords(hp1, new.coords = "cartesian")
assumedUniquePix(hp1)

sky <- CMBDataFrame(nside = 32, coords = "cartesian", ordering = "nested")
sky.s <- CMBDataFrame(sky, sample.size = 100)
hpdf <- HPDataFrame(sky.s, auto.spix = TRUE)
assumedUniquePix(hpdf)
```

baseNeighbours *Return neighbours of base pixels*

Description

The base-resolution comprises twelve pixels. baseNeighbours returns a map from the base pixel index bp to the vector of base pixels that are neighbours of bp, in counterclockwise order of direction: S,SE,E,NE,N,NW,W,SW. The presence of -1 indicates that the corresponding direction is empty.

Usage

```
baseNeighbours(bp)
```

Arguments

bp	The base pixel index

Value

A numeric vector of eight neighbouring base pixel indices in the order S, SE, E, NE, N, NW, W, SW. Missing neighbours are coded as -1. Returns NULL for an index outside 1 to 12.

Examples

```
## Return neighbours of base pixel 1
baseNeighbours(1)

## There is no base pixel 14, so baseNeighbours returns NULL
baseNeighbours(14)
```

---

cbind.CMBDataFrame *cbind for CMBDataFrames*

Description

Add a new column or columns (vector, matrix or data.frame) to a CMBDataFrame. Note that method dispatch occurs on the first argument. So, the CMBDataFrame must be the first argument

Usage

```
## S3 method for class 'CMBDataFrame'
cbind(..., deparse.level = 1)
```

Arguments

...	(generalized) vectors or matrices. Columns to bind.
deparse.level	Integer controlling the construction of labels in the case of non-matrix-like arguments.

Details

See the documentation for cbind

Value

A CMBDataFrame containing the combined columns, with HEALPix metadata and pixel indices retained from the single CMBDataFrame input.

Examples

```
cmbdf <- CMBDataFrame(nside = 1, ordering = "nested", coords = "spherical")
cmbdf2 <- cbind(cmbdf, myData = rep(1, 12))
cmbdf2
```

---

chi2CMB *Chi-squared statistic for two* CMBWindow*s*

Description

This function returns the empirical chi-squared statistic for `intensities` observations from two CMBWindows of the specified CMBDataFrame. The functions employs the function chi2.empirical and uses histogram counts of `intensities` for computations.

Usage

```
chi2CMB(cmbdf, win1, win2, intensities = "I")
```

Arguments

`cmbdf`	A CMBDataFrame.
`win1`	A CMBWindow
`win2`	A CMBWindow
`intensities`	A CMBDataFrame column with measured values.

Value

Estimated Chi-squared statistic for observations in two CMBWindows. For small sample sizes and many zero counts Chi-squared statistic is inefficient.

References

chi2.empirical

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(pi/2, pi, pi/2), phi = c(0, 0, pi/2))
chi2CMB(cmbdf, win1, win2)
```

children *Return children of a pixel*

Description

Gives four pixels at resolution $j+1$ that are contained in p, where $p$is a pixel specified at resolution j (notice it does not depend on j).

Usage

```
children(p)
```

Arguments

p	A pixel index specified in nested order.

Value

A numeric vector of four nested pixel indices at resolution $j+1$, identifying the children of pixel p.

Examples

```
children(11)
```

CMBDat *CMBDat class*

Description

The function CMBDat creates objects of class CMBDat. These are lists containing header information and other metadata as well as an element called data, whose columns may include, for example, the intensity (I), polarisation (Q, U), PMASK and TMASK. It also may contain an mmap object that points to the CMB map data table in the FITS file.

Usage

```
CMBDat(filename, mmap = FALSE, spix)
```

Arguments

filename	The path to the fits file.
mmap	A boolean indicating whether to use memory mapping.
spix	The sample pixels (rows) to read from the FITS file binary data table (optional)

Value

A list containing header information and other metadata as well as an element called `data` where: If `mmap = FALSE` then a `data.frame` is included, named `data`, whose columns may include, for example, the intensity (I), polarisation (Q, U), PMASK and TMASK. If `mmap = TRUE` then a `mmap` object is returned that points to the CMB map data table in the FITS file.

Examples

```
filename <- system.file("extdata", "CMB_testmap.fits", package = "rcosmo")
cmbdat <- CMBDat(filename, spix = 1:10)
class(cmbdat)
cmbdat$nside
cmbdat$ordering
head(cmbdat$data)
```

`CMBDataFrame` *CMBDataFrame class*

Description

The function `CMBDataFrame` creates objects of class `CMBDataFrame`. These are a special type of `data.frame` that carry metadata about, e.g., the HEALPix ordering scheme, coordinate system, and nside parameter.

Usage

```
CMBDataFrame(
  CMBData,
  coords,
  win,
  include.polar = FALSE,
  include.masks = FALSE,
  spix,
  sample.size,
  nside,
  ordering,
  I,
  ...
)
```

Arguments

`CMBData`	Can be a string location of FITS file, another `CMBDataFrame`, a `CMBDat` object, a `HPDataFrame` or unspecified.
`coords`	Can be "spherical," "cartesian", or unspecified (HEALPix only).

win	optional CMBWindow object that specifies a spherical polygon within which to subset the full sky CMB data.
include.polar	TRUE if polarisation data is required, otherwise FALSE.
include.masks	TRUE if TMASK and PMASK are required, otherwise FALSE.
spix	Optional vector of sample pixel indices, or a path to a file containing comma delimited sample pixel indices. The ordering scheme is given by ordering. If ordering is unspecified then CMBData must be either a CMBDataFrame or a FITS file and the ordering scheme is then assumed to match that of CMBData.
sample.size	If a positive integer is given, a simple random sample of size equal to sample.size will be taken from CMBData. If spix is specified then sample.size must be unspecified.
nside	Optionally specify the nside parameter manually nside=2^k (usually 1024 or 2048).
ordering	Specifies the desired HEALPix ordering scheme ("ring" or "nested") for the output CMBDataFrame. If ordering is unspecified then the ordering scheme will be taken from the CMBData object. If ordering information cannot be found the default will be "nested". This parameter also specifies the ordering scheme of spix.
I	A vector of intensities to be included if CMBData is unspecified. Note that length(I) must equal $12 * nside^2$ if either spix or sample.size are unspecified.
...	Optional names data columns of length nrow(CMBData) to add to the CMBDataFrame.

Value

A CMBDataFrame whose row.names attribute contains HEALPix indices.

Examples

```
## Construct a small synthetic sky map.
df <- CMBDataFrame(nside = 16, I = rnorm(12 * 16 ^ 2),
                   ordering = "nested")

## Take a random sample.
df.sample <- CMBDataFrame(df, sample.size = 80)
plot(df.sample)

## Select pixels by index.
df.subset <- CMBDataFrame(df, spix = c(2,4,6))

## Inspect the map and the selected pixel indices.
summary(df)

pix(df.subset)
```

CMBWindow *CMBWindow class.*

Description

The function CMBWindow creates objects of class CMBWindow. It is either a polygon or a disc type.

Usage

```
CMBWindow(..., r, set.minus = FALSE, assume.convex = FALSE)
```

Arguments

...	these arguments are compulsory and must be labelled either x, y, z (cartesian) or theta, phi (spherical, colatitude and longitude respectively). Alternatively, a single data.frame may be passed in with columns labelled x, y, z or theta, phi.
r	if a disc type window is required then this specifies the radius of the disc
set.minus	when TRUE the window will be the unit sphere minus the window specified
assume.convex	when TRUE the window is assumed to be convex resulting in a faster computation time when the window is used with functions such as subWindow. This argument is irrelevant when the window is not a polygon

Details

If r is unspecified then the rows of ... correspond to counter-clockwise ordered vertices defining a spherical polygon lying entirely within one open hemisphere on the unit sphere. Counter-clockwise is understood from the perspective outside the sphere, facing the hemisphere that contains the polygon, looking toward the origin. Note that there must be at least 3 rows (vertices) to define a polygon (we exclude bygones). On the other hand, if r is specified then ... must specify just one row, and this row is taken to be the center of a disc of radius r

Value

A data frame of class CMBWindow containing vertex coordinates for a polygon, or centre coordinates and radius r for a disc. Attributes record the coordinate system, window type and convexity assumption.

Examples

```
win <- CMBWindow(theta = c(pi/2,pi/2,pi/3, pi/3), phi = c(0,pi/3,pi/3,0))
plot(win)


## Create a disc type window
win1<- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus =TRUE)
plot(win1)
```

```
## Apply a disc type window to CMBDataFrame
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
window(cmbdf) <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus =TRUE)
plot(cmbdf)
```

`coords` *Coordinate conversion generic*

Description

Detailed descriptions and and examples can be found in documentation for specific coords functions `coords.CMBDataFrame`, `coords.CMBWindow`, `coords.HPDataFrame`, `coords.data.frame`

Usage

```
coords(x, ...)
```

Arguments

`x`	An object.
`...`	Unused arguments.

Value

A character string naming the coordinate system when it is queried, or an object of the input class with converted coordinates when a new system is supplied. See the individual methods for supported classes.

See Also

`coords.CMBDataFrame` `coords.CMBWindow` `coords.HPDataFrame` `coords.data.frame`

`coords.CMBDataFrame` *Coordinate system from a* `CMBDataFrame`

Description

If `new.coords` is unspecified then this function returns the coordinate system used in the CMBDataFrame `cmbdf`. The coordinate system is either "cartesian" or "spherical". If a new coordinate system is specified, using e.g. `new.coords = "spherical"`, then this function instead returns a new CMBDataFrame whose coordinates are of the specified type. The original CMBDataFrame, `cmbdf`, is unaffected. If you would like to change `cmbdf` without creating a new variable, then use `coords<-.CMBDataFrame` (see examples below).

Usage

```
## S3 method for class 'CMBDataFrame'
coords(x, new.coords, ...)
```

Arguments

x	A CMBDataFrame, cmbdf.
new.coords	Specifies the new coordinate system ("spherical" or "cartesian") if a change of coordinate system is desired.
...	Unused arguments.

Value

If new.coords is unspecified, then the name of the coordinate system of cmbdf is returned. Otherwise a new CMBDataFrame is returned equivalent to cmbdf but having the desired change of coordinates

Examples

```
## Create df with no coords, then create df2 with cartesian coords
df <- CMBDataFrame(nside = 16)
df
coords(df)
df2 <- coords(df, new.coords = "cartesian")
coords(df2)


## Change the coords of df directly (to spherical)
coords(df) <- "spherical"
coords(df)
```

---

coords.CMBWindow *Coordinate system from a* CMBWindow

Description

This function returns the coordinate system used in a CMBWindow. The coordinate system is either "cartesian" or "spherical"

Usage

```
## S3 method for class 'CMBWindow'
coords(x, new.coords, ...)
```

Arguments

x	a CMBWindow, win.
new.coords	specifies the new coordinate system ("spherical" or "cartesian") if a change of coordinate system is desired
...	Unused arguments.

Details

If a new coordinate system is specified, using e.g. new.coords = "spherical", the coordinate system of the CMBWindow will be converted

Value

If new.coords is unspecified, then the name of the coordinate system of win is returned. Otherwise a new CMBWindow is returned equivalent to win but having the desired change of coordinates

Examples

```
## Create win with sperical coords, then change it to win1 with cartesian coords
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
coords(win)
win1 <- coords(win, new.coords = "cartesian")
coords(win1)

## Change back to spherical coordinates

coords(win1) <- "spherical"
coords(win1)
```

---

coords.data.frame *Create a new data.frame with a given coordinate system*

Description

This does not affect the original object unless new coordinate system is directly assigned.

Usage

```
## S3 method for class 'data.frame'
coords(x, new.coords, ...)
```

Arguments

x	a data.frame with columns labelled x, y, z (for cartesian) or theta, phi (for spherical colatitude and longitude respectively)
new.coords	specifies the new coordinate system ("spherical" or "cartesian").
...	Unused arguments.

Value

A new data.frame whose coordinates are as specified by `new.coords`

Examples

```
## Create df with no coords, then create df2 with spherical coords
df <- data.frame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1))
df

df2 <- coords(df, new.coords = "spherical")
df2


## The function coords does not affect the original object.
## To change the coords assign a new value ("spherical or "cartesian")

coords(df, new.coords = "spherical")
df
coords(df) <- "spherical"
df
```

`coords.HPDataFrame` *Coordinate system from a* `HPDataFrame`

Description

Add or change coordinates in a `HPDataFrame`. This does not affect the argument object `hpdf`. Instead it returns a new `HPDataFrame` with the desired coordinates. To change `hpdf` directly see `coords<-.HPDataFrame`.

Usage

```
## S3 method for class 'HPDataFrame'
coords(x, new.coords, healpixCentered = FALSE, ...)
```

Arguments

`x`	a HPDataFrame, `hpdf`.
`new.coords`	specifies the new coordinate system ("spherical" or "cartesian")
`healpixCentered`	boolean. If TRUE then columns x,y,z or theta, phi will be ignored and removed if present. This forces the coordinates to be found from HEALPix pixel indices only. Then the HEALPixCentered attribute of `hpdf` will be set to `TRUE`.
`...`	Unused arguments.

Details

If columns exist labelled x,y,z (cartesian) or theta, phi (colatitude and longitude respectively), then these will be treated as the coordinates of `hpdf` and converted accordingly. If columns x,y,z or theta,phi are not present then the healpix pixel indices as given by `pix(hpdf)` are used for assigning coordinates.

Value

A `HPDataFrame` with columns x,y,z (cartesian) or theta, phi (colatitude and longitude respectively)

Examples

```
df <- HPDataFrame(I = rep(0,12), nside = 1)
coords(df, new.coords = "cartesian")
# Notice that df is unchanged
df

# Instead, change df directly
coords(df) <- "spherical"

## specify cartesian coordinates then convert to spherical
hp1 <- HPDataFrame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1),
                   nside = 1, auto.spix = TRUE)
hp1 <- coords(hp1, new.coords = "spherical")

## Instead, ignore/drop existing coordinates and use HEALPix only
hp2 <- HPDataFrame(x = c(1,0,0), y = c(0,1,0), z = c(0,0,1),
                   nside = 1, auto.spix = TRUE)
hp2 <- coords(hp1, new.coords = "spherical", healpixCentered = TRUE)
```

---

corrCMB *Sample correlation function*

Description

This function provides an empirical correlation function for data in a `CMBDataFrame` or data.frame. It assumes that data are from a stationary spherical random field and the correlation depends only on a geodesic distance between locations. Output is a binned correlation.

Usage

```
corrCMB(
  cmbdf,
  num.bins = 10,
  sample.size,
  max.dist = pi,
  breaks,
```

```
  equiareal = TRUE,
  calc.max.dist = FALSE
)
```

Arguments

cmbdf	is a CMBDataFrame or data.frame
num.bins	specifies the number of bins
sample.size	optionally specify the size of a simple random sample to take before calculating correlation. This may be useful if the full correlation computation is too slow.
max.dist	an optional number between 0 and pi specifying the maximum geodesic distance to use for calculating correlation. Only used if breaks are unspecified.
breaks	optionally specify the breaks manually using a vector giving the break points between cells. This vector has length num.bins since the last break point is taken as max.dist. If equiareal = TRUE then these breaks should be $cos(r_i)$ where r_i are radii. If equiareal = FALSE then these breaks should be r_i.
equiareal	if TRUE then the bins have equal spherical area. If false then the bins have equal annular widths. Default is TRUE.
calc.max.dist	if TRUE then the max.dist will be calculated from the locations in cmbdf. Otherwise either max.dist must be specified or max.dist will default to pi.

Value

#' An object of the class CMBCorrelation that is a modification of variog from the package **geoR** with variogram values replaced by correlation.

The attribute "breaks" contains the break points used to create bins. The result has num.bins + 1 values since the first value at distance 0 is not counted as a bin.

u a vector with distances.

v a vector with estimated correlation values at distances given in u.

n number of pairs in each bin

sd standard deviation of the values in each bin

bins.lim limits defining the interval spanned by each bin

ind.bin a logical vector indicating whether the number of pairs in each bin is greater or equal to the value in the argument pairs.min

var.mark variance of the data

beta.ols parameters of the mean part of the model fitted by ordinary least squares

output.type echoes the option argument

max.dist maximum distance between pairs allowed in the correlation calculations

n.data number of data

direction direction for which the correlation was computed

call the function call

References

geoR package,variog, variogramCMB, covCMB

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
corcmb <- corrCMB(cmbdf, max.dist = pi/2, num.bins = 6)
corcmb
```

---

covCMB *Sample covariance function*

Description

This function provides an empirical covariance function for data in a CMBDataFrame or data.frame. It assumes that data are from a stationary spherical random field and the covariance depends only on a geodesic distance between locations. Output is a binned covariance.

Usage

```
covCMB(
  cmbdf,
  num.bins = 10,
  sample.size,
  max.dist = pi,
  breaks,
  equiareal = TRUE,
  calc.max.dist = FALSE
)
```

Arguments

cmbdf	is a CMBDataFrame or data.frame
num.bins	specifies the number of bins
sample.size	optionally specify the size of a simple random sample to take before calculating covariance. This may be useful if the full covariance computation is too slow.
max.dist	an optional number between 0 and pi specifying the maximum geodesic distance to use for calculating covariance. Only used if breaks are unspecified.
breaks	optionally specify the breaks manually using a vector giving the break points between cells. This vector has length num.bins since the last break point is taken as max.dist. If equiareal = TRUE then these breaks should be $cos(r_i)$ where r_i are radii. If equiareal = FALSE then these breaks should be r_i.
equiareal	if TRUE then the bins have equal spherical area. If false then the bins have equal annular widths. Default is TRUE.
calc.max.dist	if TRUE then the max.dist will be calculated from the locations in cmbdf. Otherwise either max.dist must be specified or max.dist will default to pi.

Value

An object of the class CMBCovariance that is a modification of variog from the package **geoR** with variogram values replaced by covariances.

The attribute "breaks" contains the break points used to create bins. The result has `num.bins + 1` values since the first value, the sample variance, is not counted as a bin.

u a vector with distances.

v a vector with estimated covariance values at distances given in u.

n number of pairs in each bin

sd standard deviation of the values in each bin

bins.lim limits defining the interval spanned by each bin

ind.bin a logical vector indicating whether the number of pairs in each bin is greater or equal to the value in the argument pairs.min

var.mark variance of the data

beta.ols parameters of the mean part of the model fitted by ordinary least squares

output.type echoes the option argument

max.dist maximum distance between pairs allowed in the covariance calculations

n.data number of data

direction direction for which the covariance was computed

call the function call

References

geoR package, variog, variogramCMB, corrCMB

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
Cov <- covCMB(cmbdf, max.dist = pi/2, num.bins = 6)
Cov
```

`covmodelCMB` *Computes values of covariance functions*

Description

This function computes the covariances given the separation distance of locations. Options for different covariance functions on spheres are available. The function extends the function cov.spatial for additional covariance models on spheres.

Usage

```
covmodelCMB(
  obj,
  cov.model = "matern",
  cov.pars = stop("no cov.pars argument provided"),
  kappa = 0.5
)
```

Arguments

obj	Vector of distances between pairs of spatial locations.
cov.model	A type of the correlation function. Available choices are: "matern", "exponential","spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". Default is "matern"
cov.pars	A vector with two covariance parameters. The first parameter corresponds to the variance sigma^2. The second parameter corresponds to the range phi of the correlation function.
kappa	A smoothness parameter of the correlation function.

Details

The function returns the value of the covariance `C(h)` at the distance `h`. The covariance function has the form

$$C(h) = sigma^2 * rho(h/phi).$$

The parameters of the covariance are positive numbers `sigma^2`, `phi` and `kappa`.

Expressions for the correlation functions which are not included in the package **geoR**:

askey

$$rho(h/phi) = (1 - h/phi)^{kappa}, if h < phi;$$
$$0, otherwise.$$

c2wendland

$$rho(h/phi) = (1 + kappa * h/phi) * (1 - h/phi)^{kappa}, if h < phi;$$
$$0, otherwise.$$

c4wendland

$$rho(h/phi) = (1+kappa*h/phi+(kappa^2-1)*(h/phi)^2/3)*(1-h/phi)^{kappa}, if h < phi;$$
$$0, otherwise.$$

sinepower

$$rho(h/phi) = 1 - (sin(h/(2phi)))^{kappa}$$

multiquadric

$$C(h) = (1 - phi)^{(2*kappa)}/(1 + phi^2 - 2 * phi * cos(h))^{kappa}, 0 < phi < 1$$

Additional information can be found in the section Details in `cov.spatial`.

Value

Values of a covariance function for the given distances.

References

geoR package, cov.spatial

T. Gneiting. Strictly and non-strictly positive definite functions on spheres. Bernoulli 19 (2013), no. 4, 1327-1349.

Examples

```
## Compute Askey variogram at x = pi/4

1 - covmodelCMB(pi/4, cov.pars = c(1, pi), kappa = 3, cov.model = "askey" )

## Plot of the Askey covariance function

v1.f <- function(x, ...) {covmodelCMB(x, ...)}
curve( v1.f(x, cov.pars = c(1, 0.03), kappa = 3, cov.model = "askey"),
from = 0, to = 0.1, xlab = "distance", ylab = expression(cov(h)), lty = 2,
main = "covariance")
```

---

covPwSp *Covariance estimate via power spectra*

Description

This function provides a covariance estimate using the values of the estimated power spectra.

Usage

```
covPwSp(PowerSpectra, Ns)
```

Arguments

PowerSpectra	A data frame which first column lists values of multipole moments and the second column gives the corresponding values of CMB power spectra.
Ns	A number of points in which the covariance estimate is computed on the interval [-1,1]

Value

A data frame which first column is 1-d grid starting at -1+1/Ns and finishing at 1 with the step 2/Ns. The second column is the values of estimated covariances on this grid.

References

Formula (2.1) in Baran A., Terdik G. Power spectrum estimation of spherical random fields based on covariances. Annales Mathematicae et Informaticae 44 (2015) pp. 15–22.

Power Spectra data are from Planck Legacy Archive https://www.cosmos.esa.int/web/planck/pla

Examples

```
if (requireNamespace("gsl", quietly = TRUE)) {
  spectrum <- data.frame(l = 1:5, power = exp(-(1:5)))
  Cov_est <- covPwSp(spectrum, Ns = 100)
  plot(acos(Cov_est$t), Cov_est$Estimated_Cov, type = "l",
       xlab = "Angular distance", ylab = "Estimated covariance")
}
```

`displayPixelBoundaries`

Plot HEALPix pixel boundaries

Description

Plot the HEALPix pixel boundaries at `nside`

Usage

```
displayPixelBoundaries(
  nside,
  eps = pi/90,
  col = "gray",
  lwd = 1,
  ordering,
  incl.labels = 1:(12 * nside^2),
  nums.col = col,
  nums.size = 1,
  font = 2,
  depth_test = "always",
  ...
)
```

Arguments

`nside`	the HEALPix nside parameter (integer number 2^k)
`eps`	controls the smoothness of the plot, smaller eps implies more samples
`col`	the colour of plotted boundary lines
`lwd`	the thickness of the plotted boundary lines

ordering	optionally specify an ordering scheme from which to plot HEALPix pixel numbers. Can be either "ring" or "nested"
incl.labels	If ordering is specified then this parameter sets the pixel indices that will be displayed (default is all indices at nside)
nums.col	specifies the colour of pixel numbers if ordering is specified
nums.size	specifies the size of pixel numbers if ordering is specified
font	A numeric font number from 1 to 5, used if ordering is specified
depth_test	The depth test to be applied. This controls how resistant the plotted object is to being obscured. See rgl.material
...	arguments passed to rgl::plot3d

Value

Produces a plot of the HEALPix pixel boundaries.

Examples

```
displayPixelBoundaries(1, eps = pi/90, col = "red")
displayPixelBoundaries(2, eps = pi/90, col = "green")
```

---

displayPixels *Display the pixels and grandchildren*

Description

Display the pixels spix at resolution j by colouring in the grandchildren of spix at resolution $plot.j$

Usage

```
displayPixels(
  boundary.j,
  j,
  plot.j = 5,
  spix,
  boundary.col = "gray",
  boundary.lwd = 1,
  incl.labels = 1:(12 * 4^boundary.j),
  col = "blue",
  size = 3
)
```

Arguments

boundary.j	The resolution to display boundaries at. If this is missing then boundaries will not be plotted.
j	The resolution that spix are specified at.
plot.j	The resolution to plot grandchildren at
spix	Integer vector. The pixel indices to display. These must be in nested order.
boundary.col	The boundary colour.
boundary.lwd	The boundary line width.
incl.labels	Integer vector of pixel indices to label at resolution j.
col	The colour to make the grandchildren.
size	The size to make the grandchildren.

Value

No meaningful return value; called for its side effect of drawing pixels and optional boundaries in the current rgl scene.

Examples

```
## Example 1

## Plot base pixels 1,2,3 by colouring their grandchildren at resolution
## 5 (by default). No pixel boundaries.
displayPixels(j=0, spix=c(1,2,3))

## Plot base pixels 1,2,3 display and their boundaries (boundary.j=0)
displayPixels(0,0, spix=c(1,2,3))

## Plot base pixels 1,2,3 by colouring their grandchildren at resolution 2
displayPixels(0,0, plot.j = 2, spix=c(1,2,3))

## Example 2

demoNeighbours <- function(p,j) {
  neighbours(p, j)
  displayPixels(boundary.j = j, j = j, plot.j = 5,
                spix = neighbours(p, j),
                boundary.col = "gray",
                boundary.lwd = 1,
                incl.labels = neighbours(p, j),
                col = "blue",
                size = 3)
  rcosmo::displayPixelBoundaries(nside = 1, col = "blue", lwd = 3)
}

demoNeighbours(1,2)
```

`downloadCMBMap` *Download CMB Maps from Planck Public Data Release.*

Description

The function `downloadCMBMap` downloads CMB maps from https://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html.

Usage

```
downloadCMBMap(foreground = "smica", nside = 1024, destfile, release = 2)
```

Arguments

`foreground`	A string naming the foreground separation method pipeline. Please choose one of "COMMANDER", "NILC", "SEVEM" or "SMICA" (not case sensitive).
`nside`	An integer. The nside parameter (resolution) required. The available options are `1024` or `2048`.
`destfile`	A required character string with an explicit path and file name for the downloaded file. No default destination is used. Tilde-expansion is performed.
`release`	An integer. Indicates the Planck map release to download. Currently only 2 and 3 are supported.

Details

CMB maps have been produced by the COMMANDER, NILC, SEVEM, and SMICA pipelines, respectively.

For each pipeline, the intensity maps are provided at Nside = 2048, at 5 arcmin resolution, and the polarization maps are provided at Nside = 1024 at 10 arcmin resolution.

Value

The integer status code from `utils::download.file`, returned invisibly (0 indicates success). The FITS map is saved to `destfile` and can be read with `CMBDataFrame`.

References

Planck Public Data Release 2 Maps https://irsa.ipac.caltech.edu/data/Planck/release_2/all-sky-maps/matrix_cmb.html

Other fits maps can also be downloaded using the general command `download.file`.

Examples

```
## Requires internet access and downloads a large FITS file.
if (interactive()) {
  dest <- tempfile(fileext = ".fits")
  downloadCMBMap(foreground = "smica", nside = 1024, destfile = dest)
  sky <- CMBDataFrame(dest, spix = 1:10)
  unlink(dest)
}
```

`downloadCMBPS` *Download CMB Power Spectra from Planck Legacy Archive.*

Description

The function `downloadCMBPS` downloads CMB power spectra components from https://www.cosmos.esa.int/web/planck/pla.

Usage

```
downloadCMBPS(link = 1, destfile, save = TRUE)
```

Arguments

`link`	The link code (an integer from 1 to 6) for the URL to download the file. See code details in this help file.
`destfile`	A character string with an explicit path and file name. Required when `save = TRUE`; unused when `save = FALSE`. No default destination is used. Tilde-expansion is performed.
`save`	A boolean indicating whether to save or not (since the downloaded data is returned anyway).

Details

`link = 1`: Best-fit LCDM CMB power spectra from the baseline Planck TT, TE, EE+lowE+lensing (2 <= ell <= 2508).

`link = 2`: Baseline high-ell Planck TT power spectra (2 <= ell <= 2508).

`link = 3`: Baseline high-ell Planck EE power spectra (2 <= ell <= 1996).

`link = 4`: Baseline high-ell Planck TE power spectra (2 <= ell <= 1996).

`link = 5`: Low-ell Planck EB power spectra (2 <= ell <= 29).

`link = 6`: Low-ell Planck BB power spectra (2 <= ell <= 29).

Value

A data frame returned invisibly, containing multipoles in column `L` and the selected power spectrum and uncertainty columns described above. When `save = TRUE`, it is also written to `destfile`.

References

Planck Legacy Archive https://www.cosmos.esa.int/web/planck/pla

Examples

```
## Requires internet access.
if (interactive()) {
  dest <- tempfile(fileext = ".txt")
  spectrum <- downloadCMBPS(link = 6, destfile = dest)
  unlink(dest)
  spectrum <- downloadCMBPS(link = 1, save = FALSE)
  plot(spectrum$L, spectrum$TT, type = "l")
}
```

---

entropyCMB *CMB Entropy*

Description

This function returns an estimated entropy for the specified CMBDataFrame column intensities and CMBWindow region. The functions employs the function entropy and uses histogram counts of intensities for computations. All arguments of the standard entropy can be used.

Usage

```
entropyCMB(cmbdf, win, intensities = "I", method)
```

Arguments

cmbdf	A CMBDataFrame.
win	A CMBWindow
intensities	A CMBDataFrame column with measured values.
method	A method to estimate entropy, see entropy

Value

Estimated Shannon entropy for observations in CMBWindow

References

entropy

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
entropyCMB(cmbdf, win1)
```

---

exprob *Threshold exceedance probability*

Description

This function returns an estimated exceedance probability for the specified CMBDataFrame column intensities, threshold level $alpha$ and CMBWindow region.

Usage

```
exprob(cmbdf, win, alpha, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame.
win	A CMBWindow
alpha	A numeric threshold level.
intensities	The name of the column in cmbdf that contains the measured values.

Value

Estimated threshold exceedance probability

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
exprob(cmbdf, win1, alpha = mean(cmbdf$I))
```

extrCMB *Extreme values*

Description

This function returns n largest extreme values for the specified CMBDataFrame column intensities and CMBWindow region.

Usage

```
extrCMB(cmbdf, win, n, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame.
win	A CMBWindow
n	An integer value.
intensities	A CMBDataFrame column with measured values.

Value

A CMBDataFrame with n largest extreme values

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
extremes <- extrCMB(cmbdf, win1, 5)
extremes
```

fmf *First Minkowski functional*

Description

This function returns an area of the spherical region where measured values are above of the specified threshold level $alpha$.

Usage

```
fmf(cmbdf, alpha, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame.
alpha	A numeric threshold level.
intensities	A CMBDataFrame column with measured values.

Value

The area of the exceedance region

References

Leonenko N., Olenko A. (2014) Sojourn measures of Student and Fisher-Snedecor random fields. Bernoulli, 20:1454-1483.

Examples

```
n <- 64
cmbdf <- CMBDataFrame(nside=n, I = rnorm(12*n^2),
                      coords = "cartesian",
                      ordering = "nested")
fmf(cmbdf, 0, 4)
fmf(cmbdf, 2, 4)

win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
cmbdf.win <- window(cmbdf, new.window = win)
fmf(cmbdf.win, 0, 4)
```

---

fRen *Sample Renyi function*

Description

This function computes values of the sample Renyi function. Returns the estimated values of $T(q)$ for q taking values on a grid. For large data sets could be rather time consuming.

Usage

```
fRen(
  cmbdf,
  q.min = 1.01,
  q.max = 10,
  N = 20,
  k.box = log2(nside(cmbdf)) - 3,
  intensities = "I"
)
```

Arguments

cmbdf	A CMBDataFrame.
q.min	Left endpoint of the interval to compute the Renyi function. The default value is 1.01,
q.max	Right endpoint of the interval to compute the Renyi function. The default value is 10
N	Number of points to compute the Renyi function. The default value is 20.
k.box	A dyadic decomposition level in computing the Renyi function, see the references in Details. The default value is $log2(nside(cmbdf)) - 3$
intensities	A CMBDataFrame column with measured values

Value

Data frame which first column is the sampling grid $seq(q.min, q.max, length.out = N)$ of q values. Another column consists of values of the sample Renyi function $T(q)$ computed on the grid using the $k.box$th level dyadic decomposition of the unit ball.

References

(1) Leonenko, N., and Shieh, N. 2013. Rényi function for multifractal random fields. Fractals 21, Article No. 1350009.

(2) http://mathworld.wolfram.com/RenyiEntropy.html

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
Tq <- fRen(cmbdf, N = 5, k.box = 1)
plot(Tq$q, Tq$tq, xlab = "q", ylab = "Renyi function")
```

---

geo2sph *Convert geographic to spherical coordinates*

Description

Convert latitude (lat) and longitude (lon) to spherical coordinates (theta, phi) with theta in $[0, pi]$ and phi in $[0, 2 * pi)$. All values lat, lon, theta, phi are assumed to be in radians.

Usage

```
geo2sph(...)
```

Arguments

...	A data.frame with columns lat and lon, or named vectors of lat and lon.

Value

A data.frame with columns theta and phi.

Examples

```
geo <- data.frame( lat = c(0, pi/3, pi/2), lon = c(0, pi/3, pi))
geo
sph <- geo2sph(geo)
sph
```

---

geoAngle *Angle between two spherical directions*

Description

Get an angle between two directions defined by arcs on the unit sphere

Usage

```
geoAngle(p1)
```

Arguments

p1	A data.frame with rows specifying numeric points located on the unit sphere. It should have columns labelled x,y,z for Cartesian or theta, phi for spherical colatitude and longitude respectively.

Value

Let $p1[1,], p1[2,]$, and $p1[3,]$ denote the rows of p1. Then the returned object is an angle in radians beween two arcs determined by #'the pairs #'of spherical points (p1[1,], p1[2,]) and (p1[2,], p1[3,]) respectively.

Examples

```
p1 <- data.frame(diag(3))
p1
colnames(p1) <- c("x", "y", "z")
geoAngle(p1)

geo <- data.frame( lat = c(30, 0, 20), lon = c(30, 60, 10))*(pi/180)
geo
p2 <- geo2sph(geo)
p2
geoAngle(p2)
```

geoArea *geoArea generic*

Description

Detailed descriptions and and examples can be found in documentation for specific geoArea functions geoArea.CMBDataFrame, geoArea.HPDataFrame, geoArea.CMBWindow

Usage

```
geoArea(x)
```

Arguments

x	An object.

Value

A numeric scalar giving the area covered by the object on the unit sphere, in steradians.

See Also

geoArea.CMBDataFrame geoArea.HPDataFrame geoArea.CMBWindow

geoArea.CMBDataFrame *Geodesic area covered by a CMBDataFrame*

Description

Gives the surface on the unit sphere that is encompassed by all pixels in cmbdf

Usage

```
## S3 method for class 'CMBDataFrame'
geoArea(x)
```

Arguments

x	a CMBDataFrame.

Value

The sum of the areas of all pixels (rows) in x.

Examples

```
## At low resolution, a few data points can
## occupy a large pixel area, e.g.:

cmbdf <- CMBDataFrame(nside = 1, spix = c(1,2,3))
pix(cmbdf)

## The total number of Healpix points at nside=1 equals 12. As cmbdf has 3 Healpix
## it occupies pi = 1/4*(surface area of unit sphere)

geoArea(cmbdf)
plot(cmbdf, size = 5, hp.boundaries = 1)
```

---

geoArea.CMBWindow *Geodesic area of a* CMBWindow

Description

Geodesic area of a CMBWindow

Usage

```
## S3 method for class 'CMBWindow'
geoArea(x)
```

Arguments

x	A CMBWindow.

Value

The spherical area inside the CMBWindow x.

Examples

```
## A window that covers 1/8 of the unit sphere is constructed and its area is
## pi/2 = 1/8*(surface area of unit sphere)

win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
geoArea(win)
```

geoArea.HPDataFrame *Geodesic area covered by a HPDataFrame*

Description

Gives the surface on the unit sphere that is encompassed by all pixels in x.

Usage

```
## S3 method for class 'HPDataFrame'
geoArea(x)
```

Arguments

x	A HPDataFrame.

Value

The sum of the areas of all pixels (rows) in x.

Examples

```
## Generate random I for HPDataFrame
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)

## The total number of Healpix points at nside=1 equals 12. As hp1 has five
## I values at 3 Healpix points, then the occupied area is
## pi = 1/4*(surface area of unit sphere)

geoArea(hp1)
plot(hp1, size = 5, hp.boundaries = 1)
```

geoDist *Geodesic distance on the unit sphere*

Description

Get geodesic distance between points on the unit sphere

Usage

```
geoDist(p1, p2, include.names = FALSE)
```

Arguments

p1	A data.frame with rows specifying numeric points located on the unit sphere. It should have columns labelled x,y,z for Cartesian or theta, phi for spherical colatitude and longitude respectively.
p2	Same as p1.
include.names	Boolean. If TRUE then the row and column names of the returned matrix will be taken from the points in p1 and p2 (see examples below).

Value

Let n denote the number of rows of p1 and let m denote the number of rows of p2. Then the returned object is an n by m matrix whose entry in position ij is the geodesic distance from the ith row of p1 to the jth row of p2.

Examples

```
p1 <- data.frame(diag(3))
colnames(p1) <- c("x", "y", "z")
p1
p2 <- data.frame(x=c(1,0), y=c(0,3/5), z=c(0,4/5))
p2
geoDist(p1, p2, include.names = FALSE)
```

---

header *Get the FITS headers from a CMBDataFrame*

Description

Get the FITS headers from a CMBDataFrame

Usage

```
header(cmbdf)
```

Arguments

cmbdf	a CMBDataFrame.

Value

The FITS headers belonging to the FITS file from which cmbdf data was imported

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
header(cmbdf)
```

healpixCentered *Check if object is assumed to have HEALPix centered coordinates*

Description

The function checks object's attribute healpixCentered. The attribute is TRUE if the object was assumed to have rows that correspond to unique HEALPix pixel indices.

Usage

```
healpixCentered(obj)
```

Arguments

obj	Any object.

Value

A boolean. This is TRUE if obj is a CMBDataFrame or a HPDataFrame whose coordinates were assumed to correspond to HEALPix pixel center locations.

Examples

```
hp1 <- HPDataFrame(I=rnorm(5), nside = 1, spix = c(1,1,2,2,3))
pix(hp1)
coords(hp1, new.coords = "cartesian")
healpixCentered(hp1)

sky <- CMBDataFrame(nside = 32, coords = "cartesian", ordering = "nested")
sky.s <- CMBDataFrame(sky, sample.size = 100)
hpdf <- HPDataFrame(sky.s, auto.spix = TRUE)
healpixCentered(hpdf)
```

HPDataFrame *HPDataFrame class*

Description

HPDataFrames are a type of data.frame designed to carry data located on the unit sphere. Each row of a HPDataFrame is associated with a HEALPix pixel index. The HPDataFrame also holds an attribute called nside which stores the HEALPix Nside parameter (i.e., the resolution of the HEALPix grid that is being used). Unlike CMBDataFrame, HPDataFrames may have repeated pixel indices. They are made this way so that multiple data points falling within a given pixel can be stored in different rows of any given HPDataFrame.

Usage

```
HPDataFrame(
  ...,
  nside,
  ordering = "nested",
  auto.spix = FALSE,
  spix,
  assumedUniquePix = FALSE,
  delete.duplicates = FALSE,
  save.dots = FALSE,
  save.duplicate.indices = FALSE
)
```

Arguments

`...`	Data. Can be named vectors or a data.frame. May include columns (x,y,z) or (theta, phi) representing Cartesian or spherical coordinates of points on the unit sphere.
`nside`	Integer number 2^k, the nside parameter, i.e, resolution. If `nside` is unspecified, then the an attempt is made to use columns x,y and z from the provided data, as Cartesian coordinates, to calculate an nside that is sufficient to ensure all points belong to unique pixels.
`ordering`	The HEALPix ordering scheme ("ring" or "nested").
`auto.spix`	Boolean. If TRUE then spix will be found from the coordinates provided in the data. That is, each row of data will be assigned the pixel index of its closest HEALPix pixel center. There must be columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. If `auto.spix = FALSE` then `nside` must be specified.
`spix`	A vector of HEALPix pixel indices indicating the pixel locations of the data. Note that `spix` is ignored if `auto.spix = TRUE`.
`assumedUniquePix`	A boolean. Sets the `assumedUniquePix` attribute of the HPDataFrame. This attribute indicates whether or not the rows of a HPDataFrame can be assumed to belong to unique pixels.
`delete.duplicates`	Boolean. If TRUE then rows corresponding to duplicate pixel indices will be dropped from the returned HPDataFrame, and assumedUniquePix will be set to TRUE.
`save.dots`	A logical. If `TRUE` then the dot product of each observation with the nearest child HEALPix pixel center will be stored as a column called "distance" in the returned `HPDataFrame`, provided that `auto.spix = TRUE`. Note that a 'child' pixel is any one of the four pixels contained in the current pixel, in the nested scheme, at the next highest resolution. See `children`.
`save.duplicate.indices`	A logical. If `TRUE` and `delete.duplicates` is also `TRUE`, then the row indices of duplicated pixels will be retained as an attribute called "duplicates". Note

that row index refers to the row position of the duplicated pixel in the original HPDataFrame, and not the actual pixel index itself.

Details

HPDataFrame with auto.spix = TRUE can be used to transform any spherical data (not necessarily CMB) to the Healpix representation, see Example 3 below.

Value

A data frame of class HPDataFrame containing the supplied observations and any coordinate columns. HEALPix pixel indices are stored in the pix attribute; further attributes record nside, ordering and whether indices are assumed unique.

Examples

```
hp <- HPDataFrame(I = c(1, 2, 3), nside = 1, spix = c(1, 1, 2))
pix(hp)
assumedUniquePix(hp)
coords(hp, new.coords = "cartesian")

## Assign pixels automatically from three distinct locations.
hp.unique <- HPDataFrame(x = c(1, 0, 0), y = c(0, 1, 0), z = c(0, 0, 1),
                         auto.spix = TRUE)
pix(hp.unique)
assumedUniquePix(hp.unique)
```

---

ibp2p *Computes pixel's index using its subindex within base resolution*

Description

Find the pixel index p of a given pixel with index ibp in base pixel bp.

Usage

```
ibp2p(ibp, bp, j)
```

Arguments

ibp	The pixel index within base pixel bp, at resolution j, in nested order.
bp	The base pixel index
j	The resolution parameter nside = 2^j

Value

A numeric vector of full-sky nested pixel indices at resolution j, combining the within-base indices and base pixel indices.

Examples

```
ibp2p(1, 1, 2)
ibp2p(1, 2, 2)
```

`is.CMBDat` *Check if an object is of class CMBDat*

Description

Check if an object is of class CMBDat

Usage

```
is.CMBDat(cmbdf)
```

Arguments

`cmbdf`	Any R object

Value

TRUE if `cmbdf` is a CMBDat object, otherwise FALSE

Examples

```
filename <- system.file("extdata", "CMB_testmap.fits", package = "rcosmo")
cmbdat <- CMBDat(filename, spix = 1:10)
is.CMBDat(cmbdat)
```

`is.CMBDataFrame` *Check if an object is of class CMBDataFrame*

Description

Check if an object is of class CMBDataFrame

Usage

```
is.CMBDataFrame(cmbdf)
```

Arguments

`cmbdf`	Any R object

Value

TRUE if cmbdf is a CMBDataFrame, otherwise FALSE

Examples

```
df <- CMBDataFrame(nside = 16)
is.CMBDataFrame(df)
df2 <- coords(df, new.coords = "cartesian")
is.CMBDataFrame(df2)
```

---

is.CMBWindow *Check if an object is a CMBWindow*

Description

Check if an object is a CMBWindow

Usage

```
is.CMBWindow(win)
```

Arguments

win	any object

Value

TRUE or FALSE depending if win is a CMBWindow

Examples

```
win <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus = TRUE)
is.CMBWindow(win)
```

is.HPDataFrame *Check if an object is of class* HPDataFrame

Description

Check if an object is of class HPDataFrame

Usage

```
is.HPDataFrame(hpdf)
```

Arguments

hpdf	Any R object

Value

TRUE if hpdf is a HPDataFrame, otherwise FALSE

Examples

```
df <- CMBDataFrame(nside = 16)
is.HPDataFrame(df)

df <- HPDataFrame(I = rep(0,12), nside = 1)
is.HPDataFrame(df)
```

linesCMB *Adds lines of fitted variograms to variogram plots*

Description

This function adds a line with the variogram model fitted by the function variofitCMB to a current variogram plot. The function modifies lines.variomodel.variofit from the package **geoR** for additional covariance models on spheres.

Usage

```
linesCMB(x, max.dist, scaled = FALSE, ...)
```

Arguments

x	An object of the class variofit containing information about the fitted model obtained as an output of the function variofitCMB.
max.dist	A maximum distance to draw the variogram line. The default is x$max.dist.
scaled	logical. If TRUE the sill in the plot is 1.
...	other plotting parameters passed to curve

Details

The function adds a line with fitted variogram model to a plot. It is used to compare empirical variograms against fitted models returned by variofitCMB.

Available models are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric".

Value

A line with a fitted variogram model is added to a plot.

References

geoR package, lines.variomodel.variofit, covmodelCMB, variofitCMB

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
varcmb <- variogramCMB(cmbdf, max.dist = pi/2, num.bins = 6)
ols <- variofitCMB(varcmb, ini.cov.pars = c(1, 0.5),
                   cov.model = "matern", weights = "equal", messages = FALSE)
plot(varcmb)
linesCMB(ols, lty = 2)
```

---

maxDist *Get the maximum geodesic distance between points*

Description

Get the maximum geodesic distance either between all points in a data.frame pairwise, or between all points in a data.frame and one target point.

Usage

```
maxDist(df, point)
```

Arguments

df	A data.frame with columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. The rows must correspond to points on the unit sphere. If this is a HPDataFrame or CMBDataFrame and coordinate columns are missing, then coordinates will be assigned based on HEALPix pixel indices.
point	An optional target point on the unit sphere in cartesian coordinates, in which case all distances are calculated between point and the points in df.

Value

If point is specified: the longest geodesic distance from point to the points specified by the rows of df. If point is not specified: the longest geodesic distance pairwise between points in df.

Examples

```
## Using a CMBDataFrame with HEALPix coordinates only
cmbdf <- CMBDataFrame(nside = 1, spix = c(1,5,12), ordering = "ring")
plot(cmbdf, hp.boundaries = 1, col = "blue", size = 5)
p <- c(0,0,1)
maxDist(cmbdf, p) # no need to have coordinates

## Using a HPDataFrame with HEALPix coordinates only
hp <- HPDataFrame(nside = 1, I = rep(0,3), spix = c(1,5,12) )
maxDist(hp, p) # notice no need to have coordinates

## Using a data.frame with cartesian coordinates
coords(hp) <- "cartesian"
df <- data.frame(x = hp$x, y = hp$y, z = hp$z)
maxDist(df, p)

## Using a data.frame with spherical coordinates
coords(hp) <- "spherical"
df <- data.frame(theta = hp$theta, phi = hp$phi)
maxDist(df, p)

## max distance between points in cmdf
maxDist(cmbdf)
```

---

maxWindowDist *Get the maximum distance between all points in a CMBWindow*

Description

Get the maximum distance between all points in a CMBWindow

Usage

```
maxWindowDist(x)
```

Arguments

x	A CMBWindow object.

Value

The maximum distance between window's points.

Examples

```
## win is a equilateral spherical triangle which sides are pi/2
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
maxWindowDist(win)
```

`minDist` *Get the minimum geodesic distance between points*

Description

Get the minimum geodesic distance either between all points in a data.frame pairwise, or between all points in a data.frame and one target point.

Usage

```
minDist(df, point)
```

Arguments

`df`	A `data.frame` with columns x,y,z for cartesian or theta, phi for spherical colatitude and longitude respectively. The rows must correspond to points on the unit sphere. If this is a `HPDataFrame` or `CMBDataFrame` and coordinate columns are missing, then coordinates will be assigned based on HEALPix pixel indices.
`point`	An optional target point on the unit sphere in cartesian coordinates, in which case all distances are calculated between `point` and the points in `df`.

Value

If `point` is specified: the shortest distance from `point` to the points specified by the rows of `df`. If `point` is not specified: the shortest distance pairwise between points in `df`.

Examples

```
## Using a CMBDataFrame with HEALPix coordinates only
cmbdf <- CMBDataFrame(nside = 1, spix = c(1,5,12), ordering = "ring")
plot(cmbdf, hp.boundaries = 1, col = "blue", size = 5)
p <- c(0,0,1)
minDist(cmbdf, p) # no need to have coordinates

## Using a HPDataFrame with HEALPix coordinates only
hp <- HPDataFrame(nside = 1, I = rep(0,3), spix = c(1,5,12) )
minDist(hp, p) # notice no need to have coordinates

## Using a data.frame with cartesian coordinates
coords(hp) <- "cartesian"
df <- data.frame(x = hp$x, y = hp$y, z = hp$z)
minDist(df, p)
```

```
## Using a data.frame with spherical coordinates
coords(hp) <- "spherical"
df <- data.frame(theta = hp$theta, phi = hp$phi)
minDist(df, p)

## min distance between points in cmdf
minDist(cmbdf)
```

---

neighbours *Return neighbouring pixels*

Description

Return the neighbouring pixels to a given pixel p that is specified at resolution j, in the nested order.

Usage

```
neighbours(p, j)
```

Arguments

p	Pixel index p at resolution j.
j	The resolution parameter with nside = 2^j.

Value

A numeric vector of neighbouring pixel indices in nested order at resolution `j`; directions without a neighbour are omitted. For `j > 0`, the vector also includes `p` itself. For a vector of input pixels, a list of these vectors is returned.

Examples

```
## Return the neighbouring pixels for base pixel 1
neighbours(1, 0)

## Plot the neighbouring pixels for base pixel 1
demoNeighbours <- function(p,j) {
  neighbours(p, j)
  displayPixels(boundary.j = j, j = j, plot.j = j+3,
                spix = neighbours(p, j),
                boundary.col = "gray",
                boundary.lwd = 1,
                incl.labels = neighbours(p, j),
                col = "blue",
                size = 3)
  rcosmo::displayPixelBoundaries(nside = 1, col = "blue", lwd = 3)
```

```
}

demoNeighbours(1,2)
demoNeighbours(1,0)
```

`nest2ring` *Convert nest to ring ordering*

Description

Convert from "nested" to "ring" ordering

`nest2ring` computes the HEALPix pixel index in the "ring" ordering scheme from the pixel index in the "nested" ordering scheme.

Usage

```
nest2ring(nside, pix)
```

Arguments

`nside`	is the HEALPix nside parameter.
`pix`	is the set or subset of pixel indices at nside. If pix is left blank then all pixels are converted.

Value

the output is the corresponding set of pixel in the ring ordering scheme.

Examples

```
# compute HEALPix indices in the ring ordering scheme
nside <- 8
pix <-c(1,2,23)
nest2ring(nside,pix)
```

nestSearch *Finds the closest pixel center to a point*

Description

Finds the closest HEALPix pixel center to a given `target` point, specified in Cartesian coordinates, using an efficient nested search algorithm. HEALPix indices are all assumed to be in the "nested" ordering scheme.

Usage

```
nestSearch(target, nside, index.only = FALSE, save.dots = FALSE)
```

Arguments

`target`	A data.frame, matrix or vector of Cartesian (x,y,z) coordinates for the target point. If a data.frame is used then spherical coordinates can be specified with row names theta and phi.
`nside`	An integer, the target resolution at which the resulting pixels are returned.
`index.only`	A boolean indicating whether to return only the pixel index (TRUE), or cartesian coordinates as well (FALSE).
`save.dots`	A logical. A If `TRUE` then the dot product of each observation with the nearest child HEALPix pixel center will be returned as an attribute called "dot". Note that a 'child' pixel is any one of the four pixels contained in the current pixel in the nested scheme, at the next highest resolution. See `children`.

Value

if `index.only` = `TRUE` then the output will be a HEALPix index. If `index.only` FALSE then the output is the list containing the HEALPix index and Cartesian coordinate vector of the HEALPix point closest to `target` at resolution `nside`.

Examples

```
## Find the closest HEALPix pixel center at resolution j=2 for
## the point (0.6,0.8,0)

point <- c(0.6,0.8,0)
j <- 2
cpoint <- nestSearch(point, nside = 2^j)

## Plot the closest pixel center in blue and the point (0.6,0.8,0) in red
displayPixels(j, j, plot.j=j, spix=c(cpoint$pix),
              size=5, incl.labels =FALSE)
rgl::plot3d(point[1], point[2], point[3],
            col="red", size = 5, add = TRUE)
```

```
## Repeat the above for 4 points in a data.frame
points <- data.frame(x = c(1,0,0,0.6),
                     y = c(0,1,0,0.8),
                     z = c(0,0,1,0))
points
j <- 2
cpoints <- nestSearch(points, nside = 2^j)

## Plot the closest pixel center in blue and the point (0.6,0.8,0) in red
displayPixels(j, j, plot.j=j, spix=c(cpoints$pix),
              size=5, incl.labels =FALSE)
rgl::plot3d(points[,1], points[,2], points[,3],
            col="red", size = 5, add = TRUE)
```

`nside` *nside generic*

Description

Detailed descriptions and and examples can be found in documentation for specific nside functions `nside.CMBDataFrame`, `nside.HPDataFrame`

Usage

```
nside(x)
```

Arguments

x	An object.

Value

A numeric scalar giving the HEALPix nside parameter. The corresponding full-sky grid contains `12*nside^2` pixels.

See Also

`nside.CMBDataFrame` `nside.HPDataFrame`

nside.CMBDataFrame *HEALPix Nside parameter from a CMBDataFrame*

Description

This function returns the HEALPix Nside parameter of a CMBDataFrame

Usage

```
## S3 method for class 'CMBDataFrame'
nside(x)
```

Arguments

x	A CMBDataFrame.

Value

The HEALPix Nside parameter.

Examples

```
df <- CMBDataFrame(nside = 16)
nside(df)
```

nside.HPDataFrame *HEALPix Nside parameter from a HPDataFrame*

Description

This function returns the HEALPix Nside parameter of a HPDataFrame

Usage

```
## S3 method for class 'HPDataFrame'
nside(x)
```

Arguments

x	A HPDataFrame.

Value

The HEALPix Nside parameter.

Examples

```
df <- HPDataFrame(I = rep(0,12), nside = 1)
nside(df)
```

---

numeric2col *numeric2col*

Description

Map numeric values to a colour map

Usage

```
numeric2col(
  num,
  colmap = grDevices::terrain.colors(100),
  breaks.length = length(colmap)
)
```

Arguments

num	A numeric vector. The numbers which will be mapped to colours.
colmap	A colour map. See palette.
breaks.length	A single integer. Controls the number of breaks in the discretisation of num.

Value

A character vector of colours, one for each element of num, selected from colmap according to the discretised numeric values.

Examples

```
ns <- 16
sky <- CMBDataFrame(I = rnorm(12*ns^2), nside = ns)
plot(sky, col = numeric2col(sky$I))
```

ordering *ordering generic*

Description

Detailed descriptions and and examples can be found in documentation for specific ordering functions `ordering.CMBDataFrame`, `ordering.HPDataFrame`

Usage

```
ordering(x, ...)
```

Arguments

x	An object.
...	Extra arguments.

Value

A character string, `"nested"` or `"ring"`, when queried, or an object of the input class reordered to the requested scheme.

See Also

`ordering.CMBDataFrame` `ordering.HPDataFrame`

ordering.CMBDataFrame *HEALPix ordering scheme from a CMBDataFrame*

Description

This function returns the HEALPix ordering scheme from a CMBDataFrame. The ordering scheme is either "ring" or "nested".

Usage

```
## S3 method for class 'CMBDataFrame'
ordering(x, new.ordering, ...)
```

Arguments

x	A `CMBDataFrame`.
new.ordering	Specifies the new ordering ("ring" or "nest") if a change of ordering scheme is desired.
...	Unused arguments.

Details

If a new ordering is specified, using e.g. new.ordering = "ring", the ordering scheme of the CMBDataFrame will be converted.

Value

The name of the HEALPix ordering scheme that is used in the CMBDataFrame x.

Examples

```
df <- CMBDataFrame(nside = 1, ordering = "nested")
ordering(df)
df1 <- ordering(df, new.ordering = "ring")
ordering(df1)
```

---

ordering.HPDataFrame *HEALPix ordering scheme from a HPDataFrame*

Description

This function returns the HEALPix ordering scheme from a HPDataFrame. The ordering scheme is either "ring" or "nested". If a new ordering is specified, using e.g. `new.ordering = "ring"`, the ordering scheme of the HPDataFrame will be converted.

Usage

```
## S3 method for class 'HPDataFrame'
ordering(x, new.ordering, ...)
```

Arguments

x	a HPDataFrame.
new.ordering	Specifies the new ordering ("ring" or "nest") if a change of ordering scheme is desired.
...	Unused arguments.

Value

The name of the HEALPix ordering scheme that is used in the HPDataFrame x, or a new HPDataFrame with the desired new.ordering

Examples

```
df <- HPDataFrame(I = rep(0,12), nside = 1, ordering = "nested")
ordering(df)
df1 <- ordering(df, new.ordering = "ring")
ordering(df1)
```

p2bp *Return base pixel to which pixel belongs*

Description

The base pixel to which pixel p belongs at resolution j

Usage

```
p2bp(p, j)
```

Arguments

p	The pixel index at resolution j, in nested order.
j	The resolution parameter nside = 2^j

Value

A numeric vector of base pixel indices from 1 to 12, identifying the base pixel containing each input pixel.

Examples

```
p2bp(5, 0)
p2bp(5, 1)
```

p2ibp *Return pixel index within its base pixel*

Description

Convert a pixel index p to its index within the base pixel to which p belongs

Usage

```
p2ibp(p, j)
```

Arguments

p	The pixel index at resolution j, in nested order.
j	The resolution parameter nside = 2^j

Value

A numeric vector giving the nested index of each input pixel within its base pixel at resolution `j`.

Examples

```
p2ibp(6, 0)
p2ibp(6, 1)
```

`parent` *Return index of parent pixel*

Description

Gives the pixel at resolution $j-1$ that contains p, where p is specified at resolution j (notice it does not depend on j).

Usage

```
parent(p)
```

Arguments

`p`	A pixel index specified in nested order.

Value

A numeric vector of nested pixel indices at resolution $j-1$, identifying the parent containing each input pixel.

Examples

```
parent(4)
parent(5)
```

`pix` *pix generic*

Description

Detailed descriptions and and examples can be found in documentation for specific pix functions `pix.CMBDataFrame`, `pix.HPDataFrame`

Usage

```
pix(x, ...)
```

Arguments

x	An object.
...	Extra arguments.

Value

A numeric vector of HEALPix pixel indices when queried, or an object of the input class with updated pixel indices when new indices are supplied.

See Also

pix.CMBDataFrame pix.HPDataFrame

---

pix.CMBDataFrame *HEALPix pixel indices from* CMBDataFrame

Description

If new.pix is unspecified then this function returns the vector of HEALPix pixel indices from a CMBDataFrame. If new.pix is specified then this function returns a new CMBDataFrame with the same number of rows as cmbdf, but with pix attribute new.pix. Thus, new.pix must have length equal to nrow(cmbdf).

Usage

```
## S3 method for class 'CMBDataFrame'
pix(x, new.pix, ...)
```

Arguments

x	A CMBDataFrame.
new.pix	Optional vector of pixel indices with length equal to nrow(x).
...	Unused arguments.

Value

The vector of HEALPix pixel indices or, if new.pix is specified, a new CMBDataFrame.

Examples

```
df <- CMBDataFrame(nside = 16, sample.size = 10, ordering = "nested")
pix(df)
```

pix.HPDataFrame *HEALPix pixel indices from* HPDataFrame

Description

If new.pix is unspecified then this function returns the vector of HEALPix pixel indices from a HPDataFrame. If new.pix is specified then this function returns a new HPDataFrame with the same number of rows as x, but with pix attribute new.pix. Thus, new.pix must have length equal to nrow(x).

Usage

```
## S3 method for class 'HPDataFrame'
pix(x, new.pix, ...)
```

Arguments

x	a HPDataFrame.
new.pix	optional vector of pixel indices with length equal to nrow(x)
...	Unused arguments.

Value

The vector of HEALPix pixel indices (integers) or, if new.pix is specified, a new HPDataFrame.

Examples

```
df <- HPDataFrame(I = rep(0,12), nside = 1)
pix(df)
```

pix2coords *Convert pixel indices to cartesian/spherical coordinates*

Description

Convert HEALPix pixel indices to cartesian or spherical coordinates

Usage

```
pix2coords(nside, coords = "cartesian", ordering = "nested", spix)
```

Arguments

nside	the nside parameter (integer number 2^k)
coords	'cartesian' or 'spherical' coordinates
ordering	'ring' or 'nested' ordering
spix	optional integer or vector of sample pixel indices

Value

a data.frame with columns 'x', 'y', 'z' (cartesian) or 'theta', 'phi' (spherical)

Examples

```
pix2coords(nside=1, spix=c(2,5))
pix2coords(nside=1,  coords = "spherical", spix=c(2,5))
```

---

pixelArea *Area of a HEALPix pixel*

Description

Get the area of a single HEALPix pixel

Usage

```
pixelArea(nsideObject)
```

Arguments

nsideObject	CMBDataFrame, a HPDataFrame, or an integer giving the nside parameter.

Value

the area of a single HEALPix pixel at the nside resolution of nsideObject

Examples

```
df1 <- CMBDataFrame(nside = 64,
                    coords = "cartesian",
                    ordering = "nested")
pixelArea(df1)
```

pixelWindow *Find high resolution pixels falling in a lower resolution window*

Description

Find all pixels in a higher resolution that fall within the specified pixel area at a lower resolution. All pixels are assumed to be in nested ordering.

Usage

```
pixelWindow(j1, j2, pix.j1)
```

Arguments

j1	An integer. The lower resolution, with j1 =< j2. Note that `resolution = log2(nside)`.
j2	An integer. The upper resolution.
pix.j1	An integer. The pixel index at resolution j1 within which all pixels from resolution j2 will be returned. `pix.j1` can also be a vector of non-zero pixel indices.

Value

All pixels in resolution j2 that fall within the pixel pix.j1 specified at resolution j1

Examples

```
pixelWindow(3, 3, 2)
pixelWindow(3, 4, 2)
pixelWindow(3, 5, 2)
```

plot.CMBCorrelation *Plot sample CMBCorrelation*

Description

Plots sample (empirical) correlation function. Uses `plot.variogram` from **geoR** package.

Usage

```
## S3 method for class 'CMBCorrelation'
plot(x, ...)
```

Arguments

x	An object of class CMBCorrelation.
...	Extra arguments as in `plot.variogram` passed to plot.default.

Value

Produces a plot with the sample correlation function.

References

geoR package, corrCMB, variog, plot.variogram

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
corcmb <- corrCMB(cmbdf, max.dist = pi/2, num.bins = 6)
plot(corcmb)
```

---

plot.CMBCovariance *Plot sample CMBCovariance*

Description

Plots sample (empirical) covariance function. Uses plot.variogram from **geoR** package.

Usage

```
## S3 method for class 'CMBCovariance'
plot(x, ...)
```

Arguments

x	An object of class CMBCovariance.
...	Extra arguments as in plot.variogram passed to plot.default.

Value

Produces a plot with the sample covariance function.

#' @references **geoR** package, covCMB, variog, plot.variogram

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
Cov <- covCMB(cmbdf, max.dist = pi/2, num.bins = 6)
plot(Cov)
```

`plot.CMBDataFrame` *Plot CMB Data*

Description

This function produces a plot from a `CMBDataFrame`.

Usage

```
## S3 method for class 'CMBDataFrame'
plot(
  x,
  intensities = "I",
  add = FALSE,
  sample.size,
  type = "p",
  size = 1,
  box = FALSE,
  axes = FALSE,
  aspect = FALSE,
  col,
  back.col = "black",
  labels,
  hp.boundaries = 0,
  hpb.col = "gray",
  depth_test = "less",
  lab_depth_test = "always",
  ...
)
```

Arguments

`x`	A `CMBDataFrame`.
`intensities`	The name of a column that specifies CMB intensities. This is only used if `col` is unspecified.
`add`	If TRUE then this plot will be added to any existing plot. Note that if `back.col` (see below) is specified then a new plot window will be opened and `add = TRUE` will have no effect.
`sample.size`	Optionally specifies the size of a simple random sample to take before plotting. This can make the plot less computationally intensive.
`type`	A single character indicating the type of item to plot. Supported types are: 'p' for points, 's' for spheres, 'l' for lines, 'h' for line segments from z = 0, and 'n' for nothing.
`size`	The size of plotted points.
`box`	Whether to draw a box.

axes	Whether to draw axes.
aspect	Either a logical indicating whether to adjust the aspect ratio, or a new ratio.
col	Specify the colour(s) of the plotted points.
back.col	Optionally specifies the background colour of the plot. This argument is passed to rgl::bg3d.
labels	Optionally specify a vector of labels to plot, such as words or vertex indices. If this is specified then rgl::text3d is used instead of rgl::plot3d. Then length(labels) must equal nrow(x).
hp.boundaries	Integer. If greater than 0 then HEALPix pixel boundaries at nside = hp.boundaries will be added to the plot.
hpb.col	Colour for the hp.boundaries.
depth_test	The depth test to be applied to the plotted points. This controls how resistant the plotted object is to being obscured. See rgl.material
lab_depth_test	The rgl depth test to be applied to the labels and pixel boundaries if present. See rgl.material
...	Arguments passed to rgl::plot3d.

Value

A plot of the CMB data

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
plot(cmbdf)
```

---

plot.CMBWindow *Visualise a* CMBWindow

Description

Visualise a CMBWindow

Usage

```
## S3 method for class 'CMBWindow'
plot(
  x,
  add = TRUE,
  type = "l",
  col = "red",
  size = 2,
  box = FALSE,
```

```
  axes = FALSE,
  aspect = FALSE,
  back.col,
  depth_test = "always",
  ...
)
```

Arguments

x	A CMBWindow.
add	if TRUE then this plot will be added to any existing plot. Note that if back.col (see below) is specified then a new plot window will be opened and add = TRUE will have no effect
type	a single character indicating the type of item to plot. Supported types are: 'p' for points, 's' for spheres, 'l' for lines, 'h' for line segments from z = 0, and 'n' for nothing.
col	specify the colour(s) of the plotted points
size	the size of plotted points
box	whether to draw a box
axes	whether to draw axes
aspect	either a logical indicating whether to adjust the aspect ratio, or a new ratio.
back.col	specifies the background colour of the plot. This argument is passed to rgl::bg3d.
depth_test	The depth test to be applied. This controls how resistant the plotted object is to being obscured. See rgl.material
...	arguments passed to rgl::plot3d

Value

No meaningful return value; called for its side effect of drawing the window in the current rgl scene.

Examples

```
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
win2 <- CMBWindow(theta = c(2*pi/3,3*pi/4,3*pi/4, 2*pi/3), phi = c(pi/4,pi/4,pi/3,pi/3))
plot(win1)
plot(win2)
```

`plot.HPDataFrame` *Plot HPDataFrame*

Description

This function produces a plot from a HPDataFrame. If columns x,y,z (cartesian) or theta,phi (colatitude and longitude respectively) are present in `x`, then these will be used as coordinates for plotting. Otherwise, the HEALPix indices as in `pix(x)` will be used. If HEALPix indices are used and multiple rows correspond to a single pixel index, then beware that values may be obfuscated in the plot, and all locations are pixel centers.

Usage

```
## S3 method for class 'HPDataFrame'
plot(
  x,
  intensities = "I",
  add = FALSE,
  sample.size,
  type = "p",
  size = 1,
  box = FALSE,
  axes = FALSE,
  aspect = FALSE,
  col = "blue",
  back.col = "black",
  labels,
  hp.boundaries = 0,
  hpb.col = "gray",
  depth_test = "less",
  lab_depth_test = "always",
  ...
)
```

Arguments

`x`	A HPDataFrame.
`intensities`	The column name for the data in `x` that is to be treated as intensities for plotting.
`add`	if TRUE then this plot will be added to any existing plot. Note that if `back.col` (see below) is specified then a new plot window will be opened and `add = TRUE` will have no effect
`sample.size`	optionally specifies the size of a simple random sample to take before plotting. This can make the plot less computationally intensive
`type`	a single character indicating the type of item to plot. Supported types are: 'p' for points, 's' for spheres, 'l' for lines, 'h' for line segments from z = 0, and 'n' for nothing.

size	the size of plotted points
box	whether to draw a box
axes	whether to draw axes
aspect	either a logical indicating whether to adjust the aspect ratio, or a new ratio.
col	specify the colour(s) of the plotted points
back.col	optionally specifies the background colour of the plot. This argument is passed to rgl::bg3d.
labels	optionally specify a vector of labels to plot, such as words or vertex indices. If this is specified then rgl::text3d is used instead of rgl::plot3d. Then length(labels) must equal nrow(x)
hp.boundaries	integer. If greater than 0 then HEALPix pixel boundaries at nside = hp.boundaries will be added to the plot
hpb.col	colour for the hp.boundaries
depth_test	The depth test to be applied to the plotted points. This controls how resistant the plotted object is to being obscured. This controls how resistant the plotted
lab_depth_test	The rgl depth test to be applied to the labels and pixel boundaries if present. See rgl.material
...	arguments passed to rgl::plot3d

Value

A plot of the data locations according to coordinate columns or HEALPix index

Examples

```
hpdf <- HPDataFrame(I = rep(0,12), nside = 1)
plot(hpdf, size = 5, col = "yellow", back.col = "black",
     hp.boundaries = 1)
```

---

plot.variogram *Plot sample variogram*

Description

Plots sample (empirical) variogram. Uses plot.variogram from **geoR** package. See plot.variogram for usage and arguments.

Value

Produces a plot with the sample variogram.

References

geoR package, variogramCMB, variog, plot.variogram

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
varcmb <- variogramCMB(cmbdf, max.dist = pi/2, num.bins = 6)
plot(varcmb)
```

---

plotAngDis *Plot angular scatterplots and means*

Description

For specified measurements from CMBDataFrame this function produces scatterplots and binned means versus theta and phi angles.

Usage

```
plotAngDis(cmbdf, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame object.
intensities	The name of a column of cmbdf, containing measured values.

Value

2x2 plot. The first row shows scatterplots. The second row gives barplots of the corresponding means computed over bins. The first column corresponds to the values of theta and the second one is for psi.

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
plotAngDis(cmbdf)
```

`plotcovmodelCMB` *Plot theoretical CMBCovariance*

Description

Plots theoretical covariance functions from the list defined in `covmodelCMB`

Usage

```
plotcovmodelCMB(
  cov.model = "matern",
  sigmasq = 1,
  phi = pi,
  kappa = 0.5,
  from = 0,
  to = pi,
  ...
)
```

Arguments

`cov.model`	A type of the correlation function. Available choices are: "matern", "exponential","spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"
`sigmasq`	The variance parameter as documented in `covmodelCMB`. The default is 1.
`phi`	The range parameter as documented in `covmodelCMB`. The default is `pi`.
`kappa`	A smoothness parameter of the correlation function. The default is 0.5.
`from`	A lower range of the plotting region. The default is `lb =0`
`to`	An upper range of the plotting region. The default is `ub= pi`.
`...`	optional plotting parameters.

Value

Produces a plot with the theoretical covariance function.

References

`covmodelCMB`

Examples

```
plotcovmodelCMB("matern", sigmasq = 5)
plotcovmodelCMB("askey", phi = pi/4, to  = pi/2, kappa = 4)
```

plotvariogram *Plot theoretical variogram*

Description

Plots theoretical variogram functions from the list defined in covmodelCMB

Usage

```
plotvariogram(
  cov.model = "matern",
  sigmasq = 1,
  phi = pi,
  kappa = 0.5,
  from = 0,
  to = pi,
  ...
)
```

Arguments

cov.model	A type of the variogram function. Available choices are: "matern", "exponential","spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"
sigmasq	The variance parameter as documented in covmodelCMB. The default is 1.
phi	The range parameter as documented in covmodelCMB. The default is pi.
kappa	A smoothness parameter of the variogram function. The default is 0.5.
from	A lower range of the plotting region. The default is lb =0
to	An upper range of the plotting region. The default is ub= pi.
...	optional plotting parameters.

Value

Produces a plot with the theoretical variogram.

References

covmodelCMB

Examples

```
plotvariogram("matern", sigmasq = 5)
plotvariogram("askey", phi = pi/4, to  = pi/2, kappa = 4)
```

`practicalRangeCMB` *Practical range for covariance function*

Description

This function computes the practical range for covariance functions on spheres. The function extends `practicalRange` from the package **geoR** to additional covariance models on spheres.

Usage

```
practicalRangeCMB(cov.model, phi, kappa = 0.5, correlation = 0.05, ...)
```

Arguments

`cov.model`	A type of the correlation function. Available choices are: "matern", "exponential","spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric".
`phi`	The range parameter as documented in `covmodelCMB`
`kappa`	A smoothness parameter of the correlation function.
`correlation`	A correlation threshold (default is 0.05)
`...`	other optimisation parameters

Details

The practical(effective) range for a covariance function is the distance at which a covariance function first time reaches the specified value `correlation`. For covariance functions on spheres the practical range does not exceed pi, the distance beyond which a covariance function is not defined. For the covariance functions "spherical", "askey", "c2wendland", "c4wendland" their practical ranges are equal to lengths of their support.

Value

Value of the practical range for the covariance function specified in `covmodelCMB`

References

geoR package, `practicalRange`, `covmodelCMB`

Examples

```
practicalRangeCMB(cov.model = "sinepower", phi = 0.1,  kappa = 0.5)
practicalRangeCMB(cov.model = "askey", phi = 0.1,  kappa = 0.5)
```

print.CMBDataFrame *Print CMBDataFrame*

Description

This function neatly prints the contents of a CMBDataFrame.

Usage

```
## S3 method for class 'CMBDataFrame'
print(x, ...)
```

Arguments

x	A CMBDataFrame.
...	arguments passed to print.tbl_df

Value

Prints contents of the CMB data frame to the console.

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
print(cmbdf)
```

print.HPDataFrame *Print a HPDataFrame*

Description

This function neatly prints the contents of a HPDataFrame.

Usage

```
## S3 method for class 'HPDataFrame'
print(x, ...)
```

Arguments

x	A HPDataFrame.
...	arguments passed to print.tbl_df

Value

Prints contents of the HPDataFrame to the console.

Examples

```
df <- HPDataFrame(I = rep(0,12), nside = 1, ordering = "nested")
print(df)
df
```

---

pwSpCorr *Power spectra estimate via correlation*

Description

This function provides an angular power spectra estimate using the values of the sample correlations. The approach is based on Lawson-Hanson algorithm for non-negative least squares.

Usage

```
pwSpCorr(corcmb, lmax = 20 * length(corcmb$u))
```

Arguments

corcmb	An object of the class CMBCorrelation.
lmax	A number of angular power spectra components to estimate

Value

A data frame which first column is 1-d grid of l values from 0 to lmax. The second column is estimated angular power spectra components on this grid.

References

Formula (2.1) in Baran A., Terdik G. Power spectrum estimation of spherical random fields based on covariances. Annales Mathematicae et Informaticae 44 (2015) pp. 15–22.

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
corcmb <- corrCMB(cmbdf, max.dist = pi, num.bins = 8)
pw <- pwSpCorr(corcmb, lmax = 10)
pw
```

qqnormWin *Normal QQ plot for* CMBWindow

Description

This function is a modification of standard qqnorm functions to work with CMBWindow regions.

Usage

```
qqnormWin(cmbdf, win, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame.
win	A CMBWindow
intensities	A CMBDataFrame column with measured values.

Details

qqnormWin returns a normal QQ plot of for the specified CMBDataFrame column intensities and CMBWindow region. The function automatically adds a line of a "theoretical" normal quantile-quantile plot.

Value

A list with quantile components x and y and a normal QQ plot with QQ line

References

qqnorm, qqplot, qqplotWin

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
qqnormWin(cmbdf, win1)
```

qqplotWin *Quantile-Quantile plots for* CMBWindows

Description

This function is a modification of standard qqplot functions to work with CMBWindow regions.

Usage

```
qqplotWin(cmbdf, win1, win2, intensities = "I")
```

Arguments

cmbdf	A CMBDataFrame.
win1	A CMBWindow
win2	A CMBWindow
intensities	A CMBDataFrame column with measured values.

Details

qqplotWin produces a QQ plot of quantiles of observations in two CMBWindows against each other for the specified CMBDataFrame column intensities. The function automatically adds a diagonal line.

Value

A list with quantile components x and y and a QQ plot with a diagonal line

References

qqnormWin, qqnorm, qqplot

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(pi/2, pi, pi/2), phi = c(0, 0, pi/2))
qqplotWin(cmbdf, win1, win2)
```

qstat *q-statistic*

Description

This function returns an estimated q-statistic for the specified column `intensities` in a `CMBDataFrame` and the list of `CMBWindow`s.

Usage

```
qstat(cmbdf, listwin, intensities = "I")
```

Arguments

`cmbdf`	A `CMBDataFrame`.
`listwin`	A list of `CMBWindow`s
`intensities`	A `CMBDataFrame` column with measured values.

Details

The q-statistics is used to measure spatial stratified heterogeneity and takes values in [0, 1]. It gives the percent of the variance of `intensities` explained by the stratification. 0 corresponds to no spatial stratified heterogeneity, 1 to perfect spatial stratified heterogeneity.

Value

Estimated q-statistics for observations in a list of `CMBWindow`s

References

Wang, J.F, Zhang, T.L, Fu, B.J. (2016). A measure of spatial stratified heterogeneity. Ecological Indicators. 67: 250–256.

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
win1 <- CMBWindow(theta = c(0, pi/2, pi/2), phi = c(0, 0, pi/2))
win2 <- CMBWindow(theta = c(pi/2, pi, pi/2), phi = c(0, 0, pi/2))
qstat(cmbdf, list(win1, win2))
```

rbind.CMBDataFrame *rbind for CMBDataFrames*

Description

Add a new row or rows to a CMBDataFrame. All arguments passed to ... must be CMBDataFrames. If the CMBDataFrame arguments have overlapping pixel indices then all but one of the non-unique rows will be deleted unless unsafe = TRUE. If unsafe = TRUE then a HPDataFrame will be returned instead of a CMBDataFrame.

Usage

```
## S3 method for class 'CMBDataFrame'
rbind(..., deparse.level = 1, unsafe = FALSE)
```

Arguments

...	A number of CMBDataFrames
deparse.level	See documentation for rbind.data.frame.
unsafe	A boolean. If the CMBDataFrame arguments have overlapping pixel indices then all but one of the non-unique rows will be deleted unless unsafe = TRUE. If unsafe = TRUE then a HPDataFrame will be returned instead of a CMBDataFrame.

Value

A CMBDataFrame containing the combined rows and windows, with overlapping pixel indices deduplicated. If unsafe = TRUE, returns an HPDataFrame retaining duplicate pixels instead. All inputs must have matching nside and ordering.

See Also

See the documentation for rbind

Examples

```
df <- CMBDataFrame(nside = 1, I = 1:12)

df.123 <- CMBDataFrame(df, spix = c(1,2,3))
df.123
df.234 <- CMBDataFrame(df, spix = c(2,3,4))
df.234

df.1234 <- rbind(df.123, df.234)
df.1234
class(df.1234) # A CMBDataFrame
pix(df.1234)

df.123234 <- rbind(df.123, df.234, unsafe = TRUE)
```

```
df.123234
class(df.123234) # A HPDataFrame
pix(df.123234)
```

`rcosmo` *Handling and Analysing CMB data*

Description

Handling and Analysing Spherical, Healpix and Cosmic Microwave Background data on a HEALPix grid.

Details

The package `rcosmo` offers various tools for

- Downloading and transforming Cosmic Microwave Background radiation (CMB) and spherical data
- Working with Hierarchical Equal Area isoLatitude Pixelation of a sphere (Healpix)
- Spherical geometry
- Statistical analysis of CMB and spherical data
- Visualisation of Healpix data

Most of `rcosmo` features were developed for CMB, but it can also be used for other spherical data. It contains tools for transforming spherical data in cartesian and geographic coordinates to the Healpix representation.

Update

Current updates are available through URL: https://github.com/frycast/rcosmo

BugReports

https://github.com/frycast/rcosmo/issues

Author(s)

Daniel Fryer <d.fryer@latrobe.edu.au>, Andriy Olenko <a.olenko@latrobe.edu.au>, Ming Li <Ming.Li@latrobe.edu.au>, Yuguang Wang.

See Also

Useful links:

- https://github.com/frycast/rcosmo
- Report bugs at https://github.com/frycast/rcosmo/issues

resolution *Get the arcmin resolution from a CMBDataFrame*

Description

Get the arcmin resolution from a CMBDataFrame

Usage

```
resolution(cmbdf)
```

Arguments

cmbdf	a CMBDataFrame.

Value

The arcmin resolution as specified by the FITS file where the data was sourced

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
resolution(cmbdf)
```

ring2nest *Convert ring to nest ordering.*

Description

ring2nest converts HEALPix pixel indices in the 'ring' ordering scheme to HEALPix pixel indices in the 'nested' ordering scheme.

Usage

```
ring2nest(nside, pix)
```

Arguments

nside	is the HEALPix nside parameter (integer number 2^k)
pix	is a vector of HEALPix pixel indices, in the 'ring' ordering scheme.

Value

the output is a vector of HEALPix pixel indices in the 'nested' ordering scheme.

Examples

```
## Convert (1,2,23) from ring to nest at nside = 8
nside <- 8
pix <-c(1,2,23)
ring2nest(nside,pix)
```

---

sampleCMB *Take a simple random sample from a* CMBDataFrame

Description

This function returns a CMBDataFrame which size equals to sample.size, whose rows comprise a simple random sample of the rows from the input CMBDataFrame.

Usage

```
sampleCMB(cmbdf, sample.size)
```

Arguments

cmbdf	a CMBDataFrame.
sample.size	the desired sample size.

Value

A CMBDataFrame which size equals to sample.size, whose rows comprise a simple random sample of the rows from the input CMBDataFrame.

Examples

```
df <- CMBDataFrame(nside = 16, I = rnorm(12 * 16 ^ 2), ordering = "nested")
df.sample <- sampleCMB(df, sample.size = 100)
df.sample
```

siblings *Return siblings of pixel*

Description

The siblings of pixel p are defined as the children of the parent of p. Note this is resolution independent.

Usage

```
siblings(p)
```

Arguments

p	Pixel index in nested order.

Value

An integer vector of four nested pixel indices sharing the same parent as p, including p itself.

Examples

```
siblings(11)
siblings(12)
```

sphericalHarmonics *Compute spherical harmonic values at given points on the sphere.*

Description

The function sphericalHarmonics computes the spherical harmonic values for the given 3D Cartesian coordinates.

Usage

```
sphericalHarmonics(L, m, xyz)
```

Arguments

L	The degree of spherical harmonic (L=0,1,2,...)
m	The order number of the degree-L spherical harmonic (m=-L,-L+1,...,L-1,L)
xyz	Dataframe for given points in 3D cartesian coordinates

Value

values of spherical harmonics

References

See https://en.wikipedia.org/wiki/Table_of_spherical_harmonics

It uses equation (7) in Hesse, K., Sloan, I. H., & Womersley, R. S. (2010). Numerical integration on the sphere. In Handbook of Geomathematics (pp. 1185-1219). Springer Berlin Heidelberg,

but instead of the order k=1,...,2L+1 in the book we use m=k-L-1.

Examples

```
## Calculate spherical harmonic value at
## the point (0,1,0) with L=5, m=2
point<-data.frame(x=0,y=1,z=0)
sphericalHarmonics(5,2,point)

## Calculate spherical harmonic values at
## the point (1,0,0), (0,1,0), (0,0,1) with L=5, m=2
points<-data.frame(diag(3))
sphericalHarmonics(5,2,points)
```

---

summary.CMBDataFrame *Summarise a* CMBDataFrame

Description

This function produces a summary from a CMBDataFrame.

Usage

```
## S3 method for class 'CMBDataFrame'
summary(object, intensities = "I", ...)
```

Arguments

object	A CMBDataFrame.
intensities	the name of a column specifying CMB intensities (or potentially another numeric quantity of interest)
...	Unused arguments.

Value

A summary includes window's type and area, total area covered by observations, and main statistics for intensity values

Examples

```
ns <- 16
df <- CMBDataFrame(I = rnorm(12*ns^2), nside = ns,
                   ordering = "nested")

win1 <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8)
df.sample1 <- window(df, new.window = win1)
summary(df)
```

`summary.CMBWindow` *Summarise a* `CMBWindow`

Description

This function produces a summary from a CMBWindow

Usage

```
## S3 method for class 'CMBWindow'
summary(object, ...)
```

Arguments

`object`	A CMBWindow.
`...`	Unused arguments.

Value

A summary includes window's type and area

Examples

```
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
summary(win)

win1<- CMBWindow(x=0,y=3/5,z=4/5,r=0.8, set.minus = TRUE)
summary(win1)
```

summary.HPDataFrame *Summarise a* HPDataFrame

Description

This function produces a summary from a HPDataFrame.

Usage

```
## S3 method for class 'HPDataFrame'
summary(object, intensities = "I", ...)
```

Arguments

object	A HPDataFrame.
intensities	the name of a column specifying intensities (or potentially another numeric quantity of interest)
...	Unused arguments.

Value

A summary includes window's type and area, total area covered by observations, and main statistics for intensity values

Examples

```
ns <- 2
hpdf <- HPDataFrame(I = rnorm(12*ns^2), nside = 2,
                    ordering = "nested")
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
hpdf.win <- window(hpdf, new.window = win)
summary(hpdf.win)
```

triangulate *Triangulate a polygonal* CMBWindow

Description

Triangulate a polygonal CMBWindow

Usage

```
triangulate(win)
```

Arguments

win	a CMBWindow object

Value

a list of CMBWindow polygons or minus.polygons, each having 3 vertices and representing a triangle. If winType of win does not include "minus" then these triangles have pairwise disjoint interiors and their union is equal to the original polygon, win. Otherwise, if winType of win does include "minus" the triangles are the same as for the non-minus type above, but have "minus" types.

Examples

```
## Example 1

win <- CMBWindow(theta = c(2*pi/3,3*pi/4,3*pi/4, 2*pi/3),
                 phi = c(pi/4,pi/4,pi/3,pi/3))
win
plot(win)
win1 <- triangulate(win)
win1
summary(win1[[1]])
plot(win1[[1]], add= FALSE, col="green")
plot(win1[[2]], col="blue")

## Example 2: triangilation minus-type polygon

win <- CMBWindow(theta = c(pi/5,pi/3,pi/4, pi/3, pi/5),
                 phi = c(pi/5,pi/5, pi/4 ,pi/3,pi/3), set.minus =TRUE)
win
plot(win)
summary(win)
win1 <- triangulate(win)
win1
plot(win1[[1]], add= FALSE, col="green")
plot(win1[[2]], col="blue")
plot(win1[[3]], col="yellow")
summary(win1[[1]])
summary(win1[[2]])
summary(win1[[3]])
```

---

variofitCMB *Estimates parameters of variograms*

Description

This function estimates variogram parameters by fitting a parametric model from covmodelCMB to a sample variogram. The function extends variofit from the package **geoR** to additional covariance models on spheres.

Usage

```
variofitCMB(
  vario,
  ini.cov.pars,
  cov.model,
  fix.nugget = FALSE,
  nugget = 0,
  fix.kappa = TRUE,
  kappa = 0.5,
  simul.number = NULL,
  max.dist = vario$max.dist,
  weights,
  minimisation.function,
  limits = geoR::pars.limits(),
  messages,
  ...
)
```

Arguments

vario	An object of the class variogram obtained as an output of the function variogramCMB.
ini.cov.pars	A vector with initial values for the variogram parameters. The first parameter corresponds to the variance sigma^2. The second parameter corresponds to the range phi of the correlation function.
cov.model	A type of the variogram function. Available choices are: "matern", "exponential","spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric". The default is "matern"
fix.nugget	logical. Indicates whether the nugget variance should be regarded as fixed or be estimated. The default is FALSE.
nugget	A value for the nugget parameter. Regarded as a fixed values if fix.nugget = TRUE or as a initial value for the minimization algorithm if fix.nugget = FALSE. The default is zero.
fix.kappa	logical. Indicates whether the parameter kappa should be regarded as fixed or be estimated. The default is TRUE.
kappa	A value for the smoothness parameter. Regarded as a fixed values if fix.kappa = TRUE or as a initial value for the minimization algorithm if fix.kappa = FALSE. Required not in all covariance models, see covmodelCMB. The default is 0.5.
simul.number	number of simulation. Used if vario has empirical variograms for more than one data-set (simulations). The default is NULL
max.dist	A maximum distance to fit a variogram model. The default is x$max.dist.
weights	Weights used in the loss function in the minimization algorithm.
minimisation.function	Minimization function ("optim", "nlm", "nls") to estimate the parameters.

limits	Lower and upper limits for the model parameters used in the numerical minimisation by minimisation.function = "optim".
messages	logical. Indicates whether or not status messages are printed on the screen.
...	other minimisation parameters

Details

The parameter values of a variogram function from covmodelCMB are found by numerical optimization using one of the functions: optim, nlm and nls.

The function extends variofit from the package **geoR** to additional variogram models on spheres. Available models are: "matern", "exponential", "spherical", "powered.exponential", "cauchy", "gencauchy", "pure.nugget", "askey", "c2wendland", "c4wendland", "sinepower", "multiquadric".

Additionally it rescales an empirical variogram to the range [0,1] before numerical optimisation and then transforms all obtained results to the original scale. If ini.cov.pars are not provided then the 5x5 grid (seq(0,max(vario$v),l=5), seq(0,vario$max.dist,l=5)) of initial values of sigma^2 and phi is used.

Value

An object of the class variomodel and variofit, see variofit

References

geoR package, variofit, covmodelCMB

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
varcmb <- variogramCMB(cmbdf, max.dist = pi/2, num.bins = 6)
ols <- variofitCMB(varcmb, ini.cov.pars = c(1, 0.5),
                   cov.model = "matern", weights = "equal", messages = FALSE)
ols
```

---

variogramCMB *Sample variogram*

Description

This function provides an empirical variogram for data in a CMBDataFrame or data.frame. It assumes that data are from a stationary spherical random field and the covariance depends only on a geodesic distance between locations. Output is a binned variogram.

Usage

```
variogramCMB(
  cmbdf,
  num.bins = 10,
  sample.size,
  max.dist = pi,
  breaks,
  equiareal = TRUE,
  calc.max.dist = FALSE
)
```

Arguments

cmbdf	is a CMBDataFrame or data.frame
num.bins	specifies the number of bins
sample.size	optionally specify the size of a simple random sample to take before calculating variogram. This may be useful if the full covariance computation is too slow.
max.dist	an optional number between 0 and pi specifying the maximum geodesic distance to use for calculating covariance. Only used if breaks are unspecified.
breaks	optionally specify the breaks manually using a vector giving the break points between cells. This vector has length num.bins since the last break point is taken as max.dist. If equiareal = TRUE then these breaks should be $cos(r_i)$ where r_i are radii. If equiareal = FALSE then these breaks should be r_i.
equiareal	if TRUE then the bins have equal spherical area. If false then the bins have equal annular widths. Default is TRUE.
calc.max.dist	if TRUE then the max.dist will be calculated from the locations in cmbdf. Otherwise either max.dist must be specified or max.dist will default to pi.

Value

An object of class variog specified in the package **geoR**.

The attribute "breaks" contains the break points used to create bins. The result has num.bins + 1 values since the first value at distance 0 is not counted as a bin.

u a vector with distances.

v a vector with estimated variogram values at distances given in u.

n number of pairs in each bin

sd standard deviation of the values in each bin

bins.lim limits defining the interval spanned by each bin

ind.bin a logical vector indicating whether the number of pairs in each bin is greater or equal to the value in the argument pairs.min

var.mark variance of the data

beta.ols parameters of the mean part of the model fitted by ordinary least squares

output.type echoes the option argument

max.dist maximum distance between pairs allowed in the variogram calculations

n.data number of data

direction direction for which the variogram was computed

call the function call

References

geoR package, variog, covCMB, corrCMB

Examples

```
set.seed(1)
cmbdf <- CMBDataFrame(nside = 8, I = rnorm(12 * 8^2), ordering = "nested")
varcmb <- variogramCMB(cmbdf, max.dist = pi/2, num.bins = 6)
varcmb
```

---

window *window generic*

Description

Detailed descriptions and and examples can be found in documentation for specific window functions window.CMBDataFrame, window.HPDataFrame, window.data.frame

Usage

```
window(x, ...)
```

Arguments

x	An object.
...	Extra arguments.

Value

The stored window (a CMBWindow, a list of windows, or NULL for full sky) when queried, or an object of the input class restricted to the requested sky region. See the individual methods.

See Also

window.CMBDataFrame window.HPDataFrame window.data.frame

`window.CMBDat` *Get a sub window from a* `CMBDat` *object*

Description

This function returns a data.frame containing the data in `x` restricted to the CMBWindow `new.window`

Usage

```
## S3 method for class 'CMBDat'
window(x, new.window, intersect = TRUE, ...)
```

Arguments

`x`	a `CMBDat` object.
`new.window`	A single `CMBWindow` object or a list of them.
`intersect`	A boolean that determines the behaviour when `new.window` is a list containing BOTH regular type and "minus" type windows together (see details).
`...`	Unused arguments.

Details

Windows that are tagged with `set.minus` (see `CMBWindow`) are treated differently from other windows.

If the argument is a list of CMBWindows, then interious of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that `intersect = TRUE` (the default), the returned data.frame will be the points of `cmbdat$data` in the the intersection of A and B. Otherwise, if `intersect = FALSE`, the returned data.frame consists of the points of `x$data` in the union of A and B.

Note that if A (resp. B) is empty then the returned data.frame will be the points of `x` in B (resp. A).

Value

A CMBDataFrame containing the data in `x` restricted to the CMBWindow `new.window`

Examples

```
filename <- system.file("extdata", "CMB_testmap.fits", package = "rcosmo")
cmbdat <- CMBDat(filename)
win <- CMBWindow(x = 0, y = 0, z = 1, r = pi/2)
cmbdat.win <- window(cmbdat, new.window = win)
class(cmbdat.win)
```

`window.CMBDataFrame` *Get a sub window from* `CMBDataFrame`

Description

When new.window or in.pixels is unspecified this function returns the `CMBWindow` attribute of a CMBDataFrame. The return value is NULL if the window is full sky. When new.window is specified this function instead returns a new CMBDataFrame whose CMBWindow attribute is new.window

Usage

```
## S3 method for class 'CMBDataFrame'
window(x, new.window, intersect = TRUE, in.pixels, in.pixels.res = 0, ...)
```

Arguments

`x`	A `CMBDataFrame`.
`new.window`	Optionally specify a new window in which case a new CMBDataFrame is returned whose CMBWindow is new.window. `new.window` may also be a list (see details section and examples).
`intersect`	A boolean that determines the behaviour when `new.window` is a list containing BOTH regular type and "minus" type windows together (see details).
`in.pixels`	A vector of pixels at resolution `in.pixels.res` whose union contains the window(s) `new.window` entirely, or if `new.window` is unspecified then this whole pixel is returned.
`in.pixels.res`	An integer. Resolution (i.e., j such that nside = `2^j`) at which the `in.pixels` parameter is specified
`...`	Unused arguments.

Details

Windows that are tagged with `set.minus` (see `CMBWindow`) are treated differently from other windows.

If the argument `new.window` is a list of CMBWindows, then interious of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that `intersect = TRUE` (the default), the returned CMBDataFrame will be the points of `cmbdf` in the the intersection of A and B. Otherwise, if `intersect = FALSE`, the returned CMBDataFrame consists of the points of `x` in the union of A and B.

Note that if A (resp. B) is empty then the returned CMBDataFrame will be the points of `x` in B (resp. A).

Value

The window attribute of `x` or, if new.window/in.pixels is specified, a new CMBDataFrame.

Examples

```
## Example 1: Create a new CMBDataFrame with a window

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
                      ordering = "nested")
win <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
cmbdf.win <- window(cmbdf, new.window = win)
plot(cmbdf.win)
window(cmbdf.win)

## Example 2: Change the window of an existing CMBDataFrame

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
window(cmbdf) <- win2 <- CMBWindow(theta = c(pi/6,pi/3,pi/3, pi/6),
                                   phi = c(0,0,pi/6,pi/6))
plot(cmbdf)

## Example 3: union of windows

## Create 2 windows
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
win2 <- CMBWindow(theta = c(2*pi/3,3*pi/4,3*pi/4, 2*pi/3),
                           phi = c(pi/4,pi/4,pi/3,pi/3))
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the union of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = FALSE)
plot(cmbdf.win)

## Example 4: intersection of windows

## Create 2 windows
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
win2 <- CMBWindow(theta = c(pi/4,pi/3,pi/3, pi/4),
                  phi = c(pi/4,pi/4,pi/3,pi/3))
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the intersection of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
cmbdf.win12 <- window(cmbdf.win1, new.window = win2)
plot(cmbdf.win12)
plot(win1)
plot(win2)
```

```
## Example 5: intersection of windows with "minus" type

## Create 2 windows with "minus" type
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2),
                  set.minus =TRUE)
win2 <- CMBWindow(theta = c(pi/4,pi/3,pi/3, pi/4),
                  phi = c(pi/4,pi/4,pi/3,pi/3),
                  set.minus =TRUE)
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the intersection of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2))
plot(cmbdf.win)


## Example 6: intersection of windows with different types

##Create 2 windows, one with "minus" type

win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
win2 <- CMBWindow(theta = c(pi/4,pi/3,pi/3, pi/4),
                  phi = c(pi/4,pi/4,pi/3,pi/3),
                  set.minus =TRUE)
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the intersection of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = TRUE)
plot(cmbdf.win)

## Example 7: union of windows with different types

win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2), set.minus =TRUE)
win2 <- CMBWindow(theta = c(pi/4,pi/3,pi/3, pi/4), phi = c(pi/4,pi/4,pi/3,pi/3))
plot(win1)
plot(win2)

## Create CMBDataFrame with points in the union of win1 and win2

cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian", ordering = "nested")
cmbdf.win <- window(cmbdf, new.window = list(win1, win2), intersect = FALSE)
plot(cmbdf.win)
```

window.data.frame *Get a sub window from a data.frame*

Description

This function returns a data.frame containing the data in x restricted to the CMBWindow new.window

Usage

```
## S3 method for class 'data.frame'
window(x, new.window, intersect = TRUE, ...)
```

Arguments

x	A data.frame. Must have columns labelled x,y,z specifying cartesian coordinates, or columns labelled theta, phi specifying colatitude and longitude respectively.
new.window	A single CMBWindow object or a list of them.
intersect	A boolean that determines the behaviour when new.window is a list containing BOTH regular type and "minus" type windows together (see details).
...	Unused arguments.

Details

Windows that are tagged with set.minus (see CMBWindow) are treated differently from other windows.

If the argument is a list of CMBWindows, then interiors of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that intersect = TRUE (the default), the returned data.frame will be the points of x in the the intersection of A and B. Otherwise, if intersect = FALSE, the returned data.frame consists of the points of x in the union of A and B.

Note that if A (resp. B) is empty then the returned data.frame will be the points of x in B (resp. A).

Value

A data.frame containing the data in x restricted to the CMBWindow new.window

Examples

```
win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))

cmbdf <- CMBDataFrame(nside = 4)
df2 <- coords(cmbdf, new.coords = "cartesian")
df <- as.data.frame(df2[,1:3])
df
df.win <- window(df, new.window = win1)
df.win
```

window.HPDataFrame *Get a sub window from a* HPDataFrame

Description

This function returns a HPDataFrame containing the data in hpdf restricted to the CMBWindow new.window. If the HPDataFrame has columns x,y,z or theta, phi then these will be used to determine locations with priority over the HEALPix indices in pix(hpdf) unless healpixCentered = TRUE is given. Note that if healpixCentered = TRUE then columns x,y,z or theta, phi will be discarded and replaced with pixel center locations.

Usage

```
## S3 method for class 'HPDataFrame'
window(x, new.window, intersect = TRUE, healpixCentered = FALSE, ...)
```

Arguments

x	A HPDataFrame.
new.window	Optional. A single CMBWindow object or a list of them.
intersect	A boolean that determines the behaviour when new.window is a list containing BOTH regular type and "minus" type windows together (see details).
healpixCentered	A boolean. If the HPDataFrame has columns x,y,z or theta, phi then these will be used to determine locations with priority over the HEALPix indices in pix(x) unless healpixCentered = TRUE is given. Note that if healpixCentered = TRUE then columns x,y,z or theta, phi will be discarded and replaced with pixel center locations.
...	Unused arguments.

Details

Windows that are tagged with set.minus (see CMBWindow) are treated differently from other windows.

If the argument is a list of CMBWindows, then interiors of all windows whose winType does not include "minus" are united (let A be their union) and exteriors of all windows whose winType does include "minus" are intersected, (let B be their intersection). Then, provided that intersect = TRUE (the default), the returned data.frame will be the points of df in the the intersection of A and B. Otherwise, if intersect = FALSE, the returned data.frame consists of the points of df in the union of A and B.

Note that if A (resp. B) is empty then the returned data.frame will be the points of df in B (resp. A).

Value

A HPDataFrame containing the data in x restricted to the CMBWindow new.window. Or, if new.window is unspecified, then the window attribute of x is returned instead (and may be NULL).

Examples

```
ns <- 16
hpdf <- HPDataFrame(nside = ns, I = 1:(12*ns^2))
hpdf

win1 <- CMBWindow(theta = c(0,pi/2,pi/2), phi = c(0,0,pi/2))
plot(hpdf); plot(win1)

hpdf.win <- window(hpdf, new.window = win1)
plot(hpdf.win, col = "yellow", size = 4, add = TRUE)
attributes(hpdf.win)
window(hpdf.win)
hpdf.win
```

---

winType *Get/change winType*

Description

Get/change the winType (polygon or disk) of a CMBWindow. If new.type is missing then the winType of win is returned. Otherwise, a new window is returned with winType equal to new.type. If you want to change the winType of win directly, then use winType<-, see the examples below.

Usage

```
winType(win, new.type)
```

Arguments

win	a CMBWindow object or a list of such
new.type	optionally specify a new type. Use this to change between "polygon" and "minus.polygon" or to change between "disc" and "minus.disc"

Value

If new.type is missing then the winType of win is returned. Otherwise a new window is returned with winType equal to new.type

Examples

```
win <- CMBWindow(theta = c(pi/2,pi/2,pi/3, pi/3), phi = c(0,pi/3,pi/3,0))
winType(win)

win1 <- CMBWindow(x=0,y=3/5,z=4/5,r=0.8)
winType(win1)
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
```

```
                      ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
plot(cmbdf.win1)


winType(win1) <- "minus.disc"
winType(win1)
cmbdf <- CMBDataFrame(nside = 64, coords = "cartesian",
                      ordering = "nested")
cmbdf.win1 <- window(cmbdf, new.window = win1)
plot(cmbdf.win1)
```

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